

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2006, 08:14:53 ; Search time 149 Seconds  
(without alignments)  
7509.551 Million cell updates/sec

Title: US-09-920-953-2

Perfect score: 597

Sequence: 1 gcgctgctgcagacgcgc.....agccatttcgcaccaagcc 598

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.\*  
1: /EMC Celerra\_SIDS3/prodata/2/ina/1 COMB.seq.\*  
2: /EMC Celerra\_SIDS3/prodata/2/ina/5 COMB.seq.\*  
3: /EMC Celerra\_SIDS3/prodata/2/ina/6A COMB.seq.\*  
4: /EMC Celerra\_SIDS3/prodata/2/ina/6B COMB.seq.\*  
5: /EMC Celerra\_SIDS3/prodata/2/ina/7 COMB.seq.\*  
6: /EMC Celerra\_SIDS3/prodata/2/ina/H COMB.seq.\*  
7: /EMC Celerra\_SIDS3/prodata/2/ina/PCTUS COMB.seq.\*  
8: /EMC Celerra\_SIDS3/prodata/2/ina/PP COMB.seq.\*  
9: /EMC Celerra\_SIDS3/prodata/2/ina/RE COMB.seq.\*  
10: /EMC Celerra\_SIDS3/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97.2	16.3	381	US-09-902-540-5776	Sequence 5776, Ap
2	97.2	16.3	72704	US-09-902-540-1273	Sequence 1273, Ap
C 3	46.4	7.8	4403765	US-09-103-840A-2	Sequence 2, Appli
C 4	46.4	7.8	4411529	US-09-103-840A-1	Sequence 1, Appli
5	45.2	7.6	1143	US-09-902-540-8600	Sequence 8600, Ap
6	45.2	7.6	6821	US-09-902-540-907	Sequence 907, App
7	43.4	7.3	603	US-09-902-540-14	Sequence 14, Appl
8	43.4	7.3	603	US-09-902-540-5853	Sequence 5853, Ap
9	42.8	7.2	585	US-09-902-540-3555	Sequence 3555, Ap
10	42.8	7.2	19019	US-09-902-540-1171	Sequence 1171, Ap
11	42.6	7.1	3128	US-09-744-072-1	Sequence 1, Appli
12	42.6	7.1	26896	US-09-949-016-16800	Sequence 16800, A
13	42.2	7.1	759	US-09-252-991A-11092	Sequence 11092, A
14	42	7.0	1058	US-09-452-239-11	Sequence 11, Appl
15	41.6	7.0	969	US-09-902-540-8164	Sequence 8164, Ap
16	41.6	7.0	1280	US-09-096-776B-4	Sequence 4, Appli
17	41.6	7.0	1280	US-09-923-922-4	Sequence 4, Appli
18	41.6	7.0	1280	US-10-390-553-4	Sequence 4, Appli
19	41.6	7.0	1491	US-09-082-092-9	Sequence 9, Appli
20	41.6	7.0	1491	US-09-885-722A-9	Sequence 9, Appli
21	41.6	7.0	1524	US-08-840-767-3	Sequence 3, Appli
22	41.6	7.0	1817	US-09-288-292A-45	Sequence 45, Appli
23	41.6	7.0	2887	US-09-679-298A-1	Sequence 1, Appli

24	41.6	7.0	3083	2	US-08-480-994-36	Sequence 36, Appl
25	41.6	7.0	3083	2	US-08-616-844-36	Sequence 36, Appl
26	41.6	7.0	3083	2	US-08-599-654-36	Sequence 36, Appl
27	41.6	7.0	3083	2	US-08-485-573-36	Sequence 36, Appl
28	41.6	7.0	3083	3	US-08-944-868A-36	Sequence 36, Appl
29	41.6	7.0	3083	3	US-08-944-423A-36	Sequence 36, Appl
30	41.6	7.0	3083	3	US-08-925-743-36	Sequence 36, Appl
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33	41.6	7.0	3084	3	US-08-826-246-11	Sequence 11, Appl
34	41.6	7.0	3084	3	US-08-944-495-11	Sequence 11, Appl
35	41.6	7.0	3084	3	US-09-126-640-6	Sequence 6, Appl
36	41.6	7.0	3084	3	US-08-925-588-11	Sequence 11, Appl
37	41.6	7.0	3084	3	US-09-288-292A-6	Sequence 6, Appli
38	41.6	7.0	3084	3	US-09-372-044-11	Sequence 11, Appl
39	41.6	7.0	3084	3	US-08-825-486-11	Sequence 11, Appl
40	41.6	7.0	3084	3	US-08-826-248-11	Sequence 11, Appl
41	41.6	7.0	5663	3	US-09-902-540-839	Sequence 839, App
42	41.2	6.9	3066	3	US-09-902-540-9635	Sequence 9635, Ap
43	41.2	6.9	15782	3	US-09-902-540-1094	Sequence 1094, Ap
44	41	6.9	1440	3	US-09-902-540-9640	Sequence 9640, Ap
C 45	41	6.9	15782	3	US-09-902-540-1094	Sequence 1094, Ap

## ALIGNMENTS

### RESULT 1

US-09-902-540-5776  
; Sequence 5776, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 5776  
; LENGTH: 381  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-5776

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Matches 199;	Conservative	0;	Mismatches 148;	Indels 3; Gaps 1;
QY	61	AAGAGCTGTTTGATGACCTGGCGCGCCAGAGGCATGAAGCTGGCGTTGCACCTTC	120	
Db	19	AAGATGTCTAGACAGCTGGCGCGGAGAGCGCGCGTGGAGGTCTTC	78	
QY	121	TACCATAAGGTGCTGGCTGACCCCGAGCTGCTCCCTTCCTGAGTCCCTGGACATGCAA	180	
Db	79	TACCGGAAGTGTGTCGGCGGACGATCAGTACGACCACTTCTTCGAGAGCTGGACATGGAG	138	
QY	181	GAGCAGAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTGTTTGGCGGAGCAGACCAATAC	240	
Db	139	CGCCAGGCGCGAGCAGAGCGGTTCTGACGATGTTGACGGTGGCGGCTCCACTAC	198	
QY	241	AAGGCGCAAGCATGTACGACGACACGCCCATCTGTTCAAGGGCCACGGCTCGACACAC	300	
Db	199	TCGGGCAAGGACATCGCGCGGCGCACGCGCTCTGTGTAAG	255	
QY	301	CGCCACTTTGACAAGATCAACAGTACCTTGGAGAGCGCTGCAAGAGATGGCGCTCAAG	360	
Db	256	TCGCACCTTCGACGGGTGGCGGGCCACCTGAAGGCGACGCTGGAGGAGCTGGGCGTGGCC	315	



GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: August 12, 2006, 08:17:05 ; Search time 1175 Seconds

(without alignments)

6253.622 Million cell updates/sec

Title: US-09-920-953-2

Perfect score: 597

Sequence: 1 ggcgcctcgagacgccc.....agccatttcgaccagcc 598

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*  
 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*  
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 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*  
 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*  
 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*  
 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*  
 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq.\*  
 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq.\*  
 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES.

Result No.	Score	Query Match	ID	Description
1	74.4	12.5	372	US-10-282-122A-25335
2	50.8	8.5	1694969	Sequence 25335, A
3	50	8.4	2466	Sequence 1690, Ap
4	50	8.4	9025608	Sequence 5788, Ap
5	47.6	8.0	2256646	Sequence 1, Appli
6	47.4	7.9	548	Sequence 94550, A
7	46.6	7.8	1389	Sequence 255, App
8	46.6	7.8	1389	Sequence 257, App
9	46.2	7.7	1209	Sequence 32038, A
10	46.2	7.7	1509	Sequence 264, App
11	45.8	7.7	2209	Sequence 69229, A
12	45.2	7.6	2238	Sequence 97363, A
13	45.2	7.6	3743	Sequence 1, Appli
14	44.4	7.4	1445	Sequence 35783, A
15	44.2	7.4	1000	Sequence 49, Appli
16	44.2	7.4	1377	Sequence 39791, A
17	44.2	7.4	1395	Sequence 39403, A

Sequence 39036, A  
 Sequence 235, App  
 Sequence 7459, Ap  
 Sequence 72, Appl  
 Sequence 60, Appl  
 Sequence 32926, A  
 Sequence 108376,  
 Sequence 11546, A  
 Sequence 4715, Ap  
 Sequence 23705, A  
 Sequence 30, Appl  
 Sequence 18, Appl  
 Sequence 95877, A  
 Sequence 4532, Ap  
 Sequence 419, App  
 Sequence 13, Appl  
 Sequence 13, Appl  
 Sequence 13, Appl  
 Sequence 2429, Ap  
 Sequence 1, Appli  
 Sequence 1, Appli  
 Sequence 5556, Ap  
 Sequence 215, App  
 Sequence 6685, Ap  
 Sequence 4170, Ap  
 Sequence 5, Appli  
 Sequence 3, Appli  
 Sequence 11, Appli

US-10-369-493-39036  
 US-10-389-566-235  
 US-10-437-963-7459  
 US-11-228-659-72  
 US-11-228-659-72  
 US-11-097-143-32926  
 US-11-096-588A-11546  
 US-10-425-115-108376  
 US-10-739-930-4715  
 US-10-767-701-23705  
 US-10-760-493-30  
 US-10-760-493-38  
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 US-10-156-761-4532  
 US-10-755-889-419  
 US-10-651-237-13  
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 US-10-156-761-2429  
 US-10-886-033-1  
 US-10-156-761-1  
 US-10-767-701-5556  
 US-09-968-007A-215  
 US-10-843-641A-6685  
 US-10-437-963-4170  
 US-10-485-710-5  
 US-10-485-710-3  
 US-09-452-239-11

## ALIGNMENTS

RESULT 1  
 US-10-282-122A-25335  
 Sequence 25335, Application US/10282122A  
 Publication No. US20040029129A1

GENERAL INFORMATION:  
 APPLICANT: Wang, Liangsu  
 APPLICANT: Zamudio, Carlos  
 APPLICANT: Malone, Cheryl  
 APPLICANT: Haselbeck, Robert  
 APPLICANT: Ohlsen, Kari  
 APPLICANT: Zyskind, Judith  
 APPLICANT: Wall, Daniel  
 APPLICANT: Trawick, John  
 APPLICANT: Carr, Grant  
 APPLICANT: Yamamoto, Robert  
 APPLICANT: Forsyth, R.  
 APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 FILE REFERENCE: ELITRA.034A  
 CURRENT APPLICATION NUMBER: US/10/282,122A  
 CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: 60/206,848  
 PRIOR FILING DATE: 2000-05-23  
 PRIOR APPLICATION NUMBER: 60/207,727  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: 60/230,335  
 PRIOR FILING DATE: 2000-09-06  
 PRIOR APPLICATION NUMBER: 60/230,347  
 PRIOR FILING DATE: 2000-09-09  
 PRIOR APPLICATION NUMBER: 60/242,578  
 PRIOR FILING DATE: 2000-10-23  
 PRIOR APPLICATION NUMBER: 60/253,625  
 PRIOR FILING DATE: 2000-11-27  
 PRIOR APPLICATION NUMBER: 60/257,931  
 PRIOR FILING DATE: 2000-12-22  
 PRIOR APPLICATION NUMBER: 60/267,636  
 PRIOR FILING DATE: 2001-02-09  
 PRIOR APPLICATION NUMBER: 60/269,308

;; PRIOR FILING DATE: 2001-02-16  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 78614  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 25335  
;; LENGTH: 372  
;; TYPE: DNA  
;; ORGANISM: Legionella pneumophila  
US-10-282-122A-25335

Query Match 12.5%; Score 74.4; DB 8; Length 372;  
Best Local Similarity 54.0%; Pred. No. 1e-12;  
Matches 175; Conservative 0; Mismatches 146; Indels 3; Gaps 1;  
QY 68 TGTTTATGACCTGGCGCGCAGAGGATGAAGCTGGCGGTGACACTTCTACGATA 127  
DB 14 TGTGTTGAGCGATTAGCGCGCAAAATGCCGTCAACACAGCTGTGGATATTTTCTACCGCA 73  
QY 128 AGGTGCTGCTGACCGGAGCTGCTGCCCTTCTTCAGTCCCTGGACATGCAAGACAGA 187  
DB 74 AATGCTCATGATGACAGAGTGAATTATTTTTCATGACGTGGATATGGAGCAACAAA 133  
QY 188 AGATGAAGCAGGTCAGATTTCATGAGCTTCGTGTTTGGCGGAGCAGACCAATCAAGGGCC 247  
DB 134 TCTTAAAGCAAAAGGATTTTAAACCATGTTTGGCGGACCAATCAATCAATCAATGAA 193  
QY 248 GAAGCATGTACACGACACACGCCCATCTGTTCAAGGGCCACGCGCTGGACCCGCCACT 307  
DB 194 AAGTATGCGGGAAGACATCAGCATCTACT---TGCCAGAGGCTTAAATGACTCACATG 250  
QY 308 TTGACAGATCAAGCAGTACCTTGGAGACACGCTGCAAGAGATGGCGTCAAGCAGGATG 367  
DB 251 TGGATTATGTAATCGAGCATTTAGGGGAAACCCCTTAAGGAATTTGGCGCAATGAAGAGG 310  
QY 368 TGATCCAGCACCGCGCGAGTGG 391  
DB 311 ACATTCAAGAAAGTAGTGCATCG 334

RESULT 2  
US-10-506-454-1690  
;; Sequence 1690, Application US/10506454  
;; Publication No. US20060068386A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Slesarev, Alexi I  
;; APPLICANT: Mezhevaya, Katja V  
;; APPLICANT: Polushin, Nikolai N  
;; APPLICANT: Shcherbinina, Olga V  
;; APPLICANT: Shakhova, Vera V  
;; APPLICANT: Malykh, Andrei G  
;; APPLICANT: Koz'yavkin, Sergei A  
;; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile  
;; TITLE OF INVENTION: Methanopyrus kandleri AV19 and Monophyly of Archaeal Methanogens  
;; TITLE OF INVENTION: and Methods of Use Thereof  
;; FILE REFERENCE: FID001  
;; CURRENT APPLICATION NUMBER: US/10/506,454  
;; CURRENT FILING DATE: 2004-08-31  
;; PRIOR APPLICATION NUMBER: PCT/US03/06664  
;; PRIOR FILING DATE: 2003-03-04  
;; PRIOR APPLICATION NUMBER: 60/361,742  
;; PRIOR FILING DATE: 2002-03-04  
;; NUMBER OF SEQ ID NOS: 1722  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 1690  
;; LENGTH: 1694969  
;; TYPE: DNA  
;; ORGANISM: Methanopyrus kandleri  
US-10-506-454-1690

Query Match 8.5%; Score 50.8; DB 12; Length 1694969;  
Best Local Similarity 47.5%; Pred. No. 0.0004;  
Matches 151; Conservative 0; Mismatches 167; Indels 0; Gaps 0;  
QY 115 ACCTTCTACGATAAGGTGCTGGCTGACCCGAGCTGCTGCCCTTCTTCGAGTCCCTGGAC 174  
DB 421 ACCTCCCACTGCTGCTGCCGAGGACCCGCGCTGCTGGCGGCGACGCGCCGCTGCTC 480  
QY 175 ATGCAAGAGCAGAAGATGAAGCAGTCAAGTTCATGAGCTTCGTTGTTGGCGGAGCAGAC 234  
DB 481 CTGTCGACGACGAGTTCTCCACCGCAACACGGTCTCAACACCATCCGCGACCTGCGAC 540  
QY 235 CAATACAGGGCCGAAGCATGTACGACGACACACGCCCATCTGGTCAAGGGCCACGCGCTG 294  
DB 541 GAGCGCTATCCGCGCGCGGTGACGTGCTGCTGCCCTCGTGGACATGCGTCCCCCGGCC 600  
QY 295 GACCACCGCCACTTTGACAAAGATCAAGCAGTACCTTTGGAGAGAGCCTGCAAGAGATGGCC 354

QY 53 GCGGCGCAAGAAGCTGTTTATGATACCTGGCGGCGCAGAAGCATGAAGCTGGCGGTTG 112  
DB 966058 GCATGGACAAGATGCTGTCGACGAGATGGGCGAGCTGCTGTGTGACCAACGACGGTGTAA 966117  
QY 113 ACACCTTCTACGATAAGGTGCTGGCTGACCCGAGAGCTGCTGCCCTTCTTCGAGTCCCTGG 172  
DB 966118 CCATCTCGAGGAGATGACATCGAGCACCCGCGCTGAAGATGCTGTTGGAGGTTCGCCA 966177  
QY 173 ACATCAAGAGCAGAAGATGAAGCAGAGTCAAGTTCATGAGCTTCGTTGTTGGCGGAGCAG 232  
DB 966178 AGACCGCAGGAGCAGGCTGGTACGCTACGACACGCGCTGCTGCTCGCGGTGAGC 966237  
QY 233 ACCAATCAAGGGCCGAAGCATGTACGACGACACACGCCCATCTGTTAAAGGGCCACGGCC 292  
DB 966238 TGCTGCACAAGGCCCGAGGATCTACTGTCAGCAGGACATCCACCCGCTGATCGCACGG 966297  
QY 293 TGGACACCGCCACTTTCACAAGATCAAGCAGTACCTTTGGAGAGACGCTGCAAGAGATCG 352  
DB 966298 GTTACCGAATGGCCGTCGAAAAGGCCGAGGATCTCTTTGAGGAGATCGCCGAAGAGATCG 966357  
QY 353 GCGTCAAGCAGGATGTGA 370  
DB 966358 ACCCGATGACGAGGAGA 966375

RESULT 3  
US-10-156-761-5788  
;; Sequence 5788, Application US/10156761  
;; Publication No. US20030119018A1  
;; GENERAL INFORMATION:  
;; APPLICANT: OMURA, SATOSHI  
;; APPLICANT: IKEDA, HARUO  
;; APPLICANT: ISHIKAWA, JUN  
;; APPLICANT: HORIKAWA, HIROSHI  
;; APPLICANT: SHIBA, TADAYOSHI  
;; APPLICANT: SAKAKI, YOSHIYUKI  
;; APPLICANT: HATTORI, MASAHIRA  
;; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
;; FILE REFERENCE: 249-262  
;; CURRENT APPLICATION NUMBER: US/10/156,761  
;; CURRENT FILING DATE: 2002-05-29  
;; PRIOR APPLICATION NUMBER: JP 2001-204089  
;; PRIOR FILING DATE: 2001-05-30  
;; PRIOR APPLICATION NUMBER: JP 2001-272697  
;; PRIOR FILING DATE: 2001-08-02  
;; NUMBER OF SEQ ID NOS: 15109  
;; SEQ ID NO 5788  
;; LENGTH: 2466  
;; TYPE: DNA  
;; ORGANISM: Streptomyces avermitilis  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (1)..(2466)  
US-10-156-761-5788

Query Match 8.4%; Score 50; DB 7; Length 2466;  
Best Local Similarity 47.1%; Pred. No. 9.7e-05;  
Matches 152; Conservative 0; Mismatches 171; Indels 0; Gaps 0;  
QY 115 ACCTTCTACGATAAGGTGCTGGCTGACCCGAGCTGCTGCCCTTCTTCGAGTCCCTGGAC 174  
DB 421 ACCTCCCACTGCTGCTGCCGAGGACCCGCGCTGCTGGCGGCGACGCGCCGCTGCTC 480  
QY 175 ATGCAAGAGCAGAAGATGAAGCAGTCAAGTTCATGAGCTTCGTTGTTGGCGGAGCAGAC 234  
DB 481 CTGTCGACGACGAGTTCTCCACCGCAACACGGTCTCAACACCATCCGCGACCTGCGAC 540  
QY 235 CAATACAGGGCCGAAGCATGTACGACGACACACGCCCATCTGGTCAAGGGCCACGCGCTG 294  
DB 541 GAGCGCTATCCGCGCGCGGTGACGTGCTGCTGCCCTCGTGGACATGCGTCCCCCGGCC 600  
QY 295 GACCACCGCCACTTTGACAAAGATCAAGCAGTACCTTTGGAGAGAGCCTGCAAGAGATGGCC 354





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; SEQ ID NO 32038
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Thermobifida fusca
US-10-369-493-32038

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Best Local Similarity 7.7%; Score 46.2; DB 7; Length 1209;
Matches 90; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 248 GAAGCATGTATGACGACGACACCCCATCTGGTCAAGGGCCACGGCTTGACACCGCCACT 307
DB 86 GCACCTGCTCTTCGACGAAGTGTGTGGTGGAGCGCCCGCGAGGACACACCTGT 145

QY 308 TTGACAGATCAACAGTACCTTGAGAGAGCGTGAAGAGATGGCGTCAAGCAGATG 367
DB 146 TCGTCCAGCTCTCTCGGACCGGGGTGACCGTGCATGAATTCGGCAGCCTGCTCGG 205

QY 368 TGATCCAGCAGCGCCGCGAGTGTGGAGTCCACCCGCGACGA 410
DB 206 AGACTCTGCACATCCCGAGCGAAGAGTTTCATCTCGACGA 248

RESULT 10
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; Sequence 264, Application US/10411910A
; Publication No. US20040209256A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
; FILE REFERENCE: H2041203-P
; CURRENT APPLICATION NUMBER: US/10/411,910A
; CURRENT FILING DATE: 2003-04-12
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 264
; LENGTH: 1509
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-411-910A-264

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QY 114 CACCTTCTACGATAGGTGCTGGTGAACCGGAGCTGCTGCCCTTCTTGAGTCCCTGGA 173
DB 906 CGGCGAGATCGCCCGCATCATGAGCAGGGCGACCTGAGCGTGGCGACCGCCGCTGA 965

QY 174 CATGCAAGACGACGAAGATGAAGAGGTCAAGTTTCATGAGCTTCTGGCGGACGA 233
DB 966 CACCTGTTTCGGCGACTGAAGAGGACAAAGTGAACCGCACAGCGGCCACGACGCA 1025

QY 234 CCAATCAAGGCGCGAAGCATGTACGACGACACGCCCATCTGTTCAAGGGCCACCGCCT 293
DB 1026 CGGCCACCTGGCCACATCTTCCGCCACGCGCCCAAGGAGCTGTTCAACGAGGACGTGA 1085

QY 294 GGACACCGCCACTTTGACAAGATCAAGCATGTTGAGAGACGCTTGAAGAGATGGG 353
DB 1086 GGAGGTGACCTACCGGCGCCCTTGGCGCAACAAGGACTTCCAGGAGTGCACCTGGAGAAGA 1145

QY 354 GPTCAAGCAGGATGTATCCAGCAGCGCCG 384
DB 1146 CGGCGAGGTGGTCTGCGCTTCGCGCGCCG 1176

RESULT 11
US-10-437-963-69229
; Sequence 69229, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 97363
; LENGTH: 2209
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_69918C.1
US-10-437-963-69229

Query Match
Best Local Similarity 7.7%; Score 45.8; DB 8; Length 2209;
Matches 152; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 110 TTGACACCTTCTACGATAAGGTGCTGGCTGACCCGAGCTGCTGCCCTTCTTCGAGTCCC 169
DB 400 TCGACTACGTGTGTTTACAAGGGGACCGACGACCGGAGCTCCCGACGACCTGTGGGCG 459

QY 170 TGGACATGCAAGAGCAGAGATGAAGCAGGTCAAGTTTCATGAGCTTCTGTTTGGCGGAG 229
DB 460 AGATCATCCAGCGCAACAAGCTGCTGGGCTGAGGAGTACAAGTTCTCTCAAGGTCA 519

QY 230 CAGACCAATACAGGGCCGAGCATGTAGCAGCACACCCCATCTGTTCAAGGGCCACG 289
DB 520 TCGTCAACTCCGGCATCGCGGAGAGACCTACGGGCGCGGAAACATCATCGGCGGCGG 579

QY 290 GCTGGACCAACCGCCACTTTGACAAGATCAACAGTACCTTGAGAGAGCGTCAAGAGA 349
DB 580 AGCGCGCGCCCGACCGCTCGCGGAGGATGAGGAGATGAGACGAGATTTCCACGCG 639

QY 350 TGGGGCTCAAGCAGGATGTGATCCAGCAGCGCGCGGAGTGGTGGAGTCCACCGCGAGC 409
DB 640 TCGTCGACGAGCTGTTTCGCGCGCTCGTCGCGCGCGGCGCGCGCGTCCGCGCGCG 699

QY 410 AATTTGACTTNCACCAACTCGGCACCCA 439
DB 700 ACGTCGACCTCTCGTCTGTCACAGTGTCCA 729

RESULT 12
US-10-437-963-97363/c
; Sequence 97363, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 97363
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RESULT 15  
US-10-389-566-49/c  
; Sequence 49, Application US/10389566



Search completed: August 12, 2006, 08:39:19  
Job time : 1187 secs

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2006, 08:19:39 ; Search time 186 Seconds

(without alignments)  
5105.749. Million cell updates/sec

**Title:** US-09-920-953-2

Perfect score: 597

Sequence: 1 gcgctgcctgcagacgcggc.....agccatttgcgaccaagcc 598

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

## Listing first 45 summaries

Database : Published Applications NA New:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	Score	Match	Length			
1	47.4	7.9	1791	6	US-10-449-902-20040	Sequence 20040, A
	47	7.9	1830	6	US-10-449-902-7207	Sequence 7207, Ap
	47	7.9	2261	6	US-10-449-903-25898	Sequence 25898, A
2	44.2	7.4	898	8	US-11-266-748A-371178	Sequence 371178, A
	44.2	7.4	898	8	US-11-266-748A-454557	Sequence 454557, A
	44.2	7.4	2559	9	US-11-218-305-13889	Sequence 13889, A
3	44	7.4	1676	6	US-10-449-902-10126	Sequence 10126, A
	44	7.4	1770	6	US-10-449-903-20915	Sequence 20915, A
	43.8	7.3	1451	6	US-10-953-349-29115	Sequence 29115, A
4	43.2	7.2	3618	9	US-11-056-355B-68882	Sequence 68882, A
	42.6	7.1	3487	8	US-11-218-305-17353	Sequence 17353, A
	42.2	7.1	1467	6	US-11-266-748A-57192	Sequence 57192, A
5	42	7.0	1052	6	US-10-449-903-7212	Sequence 7212, Ap
	41.6	7.0	575	8	US-11-266-748A-3647	Sequence 3647, Ap
	41.6	7.0	575	8	US-11-266-748A-63159	Sequence 63159, A
6	41.6	7.0	719	8	US-11-266-748A-65991	Sequence 65991, A
	41.6	7.0	719	8	US-11-266-748A-273645	Sequence 273645, A
	41.6	7.0	807	8	US-11-266-748A-334162	Sequence 334162, A
7	41.6	7.0	807	8	US-11-266-748A-76043	Sequence 76043, A
	41.6	7.0	807	8	US-11-266-748A-109209	Sequence 109209, A
	41.6	7.0	800	8	US-11-266-748A-128854	Sequence 128854, A
8	41.6	7.0	1000	8	US-11-266-748A-286931	Sequence 286931, A

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C	39	40.6	6.8	1327	6	US-10-449-902-10787	Sequence 10787, A
C	40	40.4	6.8	1513	6	US-10-449-902-10787	Sequence 10787, A
C	41	39.6	6.6	84428	8	US-11-330-363-1	Sequence 20335, A
C	42	39.4	6.6	1000	8	US-11-266-748A-283662	Sequence 1, Appli
C	43	39.4	6.6	1000	8	US-11-266-748A-335091	Sequence 283662,
C	44	39.4	6.6	1000	8	US-11-266-748A-335091	Sequence 335091,
C	45	39.4	6.6	1000	8	US-11-266-748A-339427	Sequence 339427,
C	46	39.4	6.6	1000	8	US-11-266-748A-464473	Sequence 464473.

## · ALIGNMENTS

RESULT 1  
US-10-449-902-20040  
; Sequence 20040, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20040  
; LENGTH: 1781  
; TYPE: DNA

Query Match	7.9%	Score 47.4;	DB 6;	Length 1781;
Best Local Similarity	50.4%	Pred. No. 0.0045;		
Matches 114;	Conservative	0;	Mismatches 112;	Indels 0;
				Gaps 0;

Qy	216	CGTGTTTGGCGGAGCAGACCAATACAAAGGCGCAAGCATGTACGACGACACGCGCCATCT	275
Db	407	CGTGTTTCGCGCGCGCCACGCCCGCTCGCGGGGGGCGATGTTCCGCGACCTTCGCCCGCTG	466
Qy	276	GGTCAAGGGCCACGGGCTGGACACCGCCACTTTGCAAGATCAAGCAGTACCTTTGGAGA	335
Db	467	CGTCATGCTCCACATGCTCAACTTTCGCGAGGCGGTGACCATGACGAGCGCGGCCCGGA	526
Qy	336	GACGTCGAAGAGATGGGGTCAAGCAGGATGTATCCAGCACGCCGCGAGTGGTGG	395
Db	527	GAAGCTCTTCAAGGTGCTCGACATGTACGAGGCCACCCGGCGACGCGTCCCGCGTATCG	586
Qy	396	GTTCACCCCGCAGAAATTGACTTTCACCAACAACTGCGCACCCCAAC	441



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Query Match
Best Local Similarity 7.4%; Score 44.2; DB 8; Length 898;
Matches 103; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 GCGCTGCTTCAGACGGCGCCACACAGAGAGCGCGGAGCGGATGCGGGCGC 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
69 GTGGTGCCACCGCGCTGCGCGCGCCAGCGCGAGCTGCTGGTGGGTGCGGGCCC 128
QY 61 AAGAAGCTGTTTGATGACCTGGCGCGCGAGAGCATGAAGCTGGGTTGACACCTTC 120
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129 GAGCTGGGCGGTGGAGCGCGCGCGCTGCTGCGCTGAGCGCGCGCGCACCGCGCG 188
QY 121 TACGATAAGTGTCTGGCTGACCGCGAGCTGCTGCCCTTCTTCGAGTCCCTGACATGCAA 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
189 GCGAGCGGGCGCTGGCGCTGAGAGCGCGGCGCTGCTGGGAGGTGGAGCTGGCG 248
QY 181 GAGCAGAAGATGAACAGGTC 201
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249 GCCGAGGAGCGCGCGCAGGAC 269

RESULT 5
US-11-266-748A-454557/c
; Sequence 454557, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 5815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 454557
; LENGTH: 898
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-454557

Query Match
Best Local Similarity 7.4%; Score 44.2; DB 8; Length 898;
Matches 103; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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830 GTGGTGCCACCGCGCTGCGCGCGCCAGCGCGAGCTGCTGGTGGGTGCGGGCCC 771
QY 61 AAGAAGCTGTTTGATGACCTGGCGCGCGAGAGCATGAAGCTGGGTTGACACCTTC 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
770 GAGCTGGGCGGTGGGAGCGCGCGGTGCTGCGCTGAGCGCGCGCGCACCGCGCG 711
QY 121 TACGATAAGTGTCTGGCTGACCGCGAGCTGCTGCCCTTCTTCGAGTCCCTGACATGCAA 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
710 GCGACGGGCGCTGGCGCTGAGAGCGCGGCGCTGTGGCTCGGGAGGTGGAGCTGGCG 651
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QY 181 GAGCAGAAGATGAAGCAGGTC 201
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650 GCCGAGGAGCGCGCGCAGGAC 630

RESULT 6
US-11-218-305-13889
; Sequence 13889, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: McLaaird, Paul L.
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
; FILE REFERENCE: 38-21 (53660)B
; CURRENT APPLICATION NUMBER: US/11/218,305
; PRIOR FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: US 60/606,880
; PRIOR FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 25043
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13889
; LENGTH: 2559
; TYPE: DNA
; ORGANISM: Zea mays
US-11-218-305-13889

Query Match
Best Local Similarity 7.4%; Score 44.2; DB 9; Length 2559;
Matches 91; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 66 GCTGTTTGATGACCTGGCGCGCGCAGAGCATGAAGCTGGCGTTGACACCTTCTACGA 125
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1434 GCAGTTCATCGCCGCGTCCACCGCGCGAGATGCTCAGCGTAGAGGCTTACACGA 1493
QY 126 TAAGGTGCTGCTGACCCCGAGGCTGCTGCCCTTCTTCGAGTCCCTGGACATGCAAGAGCA 185
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1494 CATCGTGTGCGCGAGGCGCGTGTCCGCGCGGAGATCTCTGGTGGTGCACCGCCCC 1553
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1554 GAGCTCAAGAGTCGAGGAGGTGGCGCGCTGGTGTCTGTCGCCGAC 1602

RESULT 7
US-10-449-902-10126/c
; Sequence 10126, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10126
; LENGTH: 1676
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK107474
; DATABASE ENTRY DATE: 2002-08-28
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OTHER INFORMATION: Ceres Seq. ID no. 13655338  
US-11-056-355B-68892

Query Match 7.3%; Score 43.8; DB 9; Length 1451;  
Best Local Similarity 56.2%; Pred. No. 0.04;  
Matches 81; Conservative 0; Mismatches 63; Indels 0; Gaps 0;  
QY 285 CCAGGCTGACACCGCCACTTTCAGAGATCAAGCAGTACCTTGGAGAGACGCTGCA 344  
Db 291 CTTGCTCCAGTTCGGGACCTCGCTGACCGCCAGCGCTGGCGTGAGAGATCCTGCG 350  
QY 345 AGAGATGGCGCTCAAGCAGGATGTATCCAGCAGCGCCCGGAGTGGTGGATCCACCG 404  
Db 351 CGAGATCGGCTCAAGTTCGGGAGATCCAGAACGAGGCGCTCGGGGAGACCGGCTCCG 410  
QY 405 CGAGCAATTTGACTTNNCCCAAA 428  
Db 411 AGACTCAACGACGAGATCAACAA 434

## RESULT 11

US-11-218-305-17353  
; Sequence 17353, Application US/11218305  
; Publication No. US2006014195A1  
; GENERAL INFORMATION:  
; APPLICANT: MONSANTO TECHNOLOGY, LLC  
; APPLICANT: McLaaird, Paul L.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Wu, Kunsheng  
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping  
; FILE REFERENCE: 38-21 (53660)B  
; CURRENT APPLICATION NUMBER: US/11/218,305  
; CURRENT FILING DATE: 2005-09-01  
; PRIOR APPLICATION NUMBER: US 60/606,880  
; PRIOR FILING DATE: 2004-09-01  
; NUMBER OF SEQ ID NOS: 25043  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 17353  
; LENGTH: 3618  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1640)..(1640)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1733)..(1733)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1885)..(1885)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1908)..(1908)  
; OTHER INFORMATION: n is a, c, g, or t

## US-11-218-305-17353

Query Match 7.2%; Score 43.2; DB 9; Length 3618;  
Best Local Similarity 46.9%; Pred. No. 0.084;  
Matches 135; Conservative 0; Mismatches 153; Indels 0; Gaps 0;  
QY 2 CGTGTCTGACAGCGGCCACACAGACCGCGGAGCGGATGCGGGCGCA 61  
Db 2652 CGCGCGCGGTACCGGAAGACGCGTCCACGCGCGCGGCGGAGCGGAGGACCA 2711  
QY 62 AGAAGCTGTTTGTATGACTCGGGCGCGCAGAGGCGATGAAGCTGGCGTTGACACCTTCT 121  
Db 2712 ATATATAGGCGGAGGAGCTCAGGAGGAGGAGGCGCTGTATCGTGAAGGTGAGCATGAGC 2771  
QY 122 ACGATAAGGTGCTGGTGTACCGGAGCTGTGCTTCTTCGAGTCCCTGGACATGCAAG 181

Db 2772 GGGCGCCATACCTCCGAAGGTGACCTGCGGACCTAGCGGCGCTACCGTGAGCTGAGGG 2831  
QY 182 AGCAGAGATCAAGCAGGTCAAGTTTCATGAGCTTCGTTTGGGGGAGCAGACCAATACA 241  
Db 2832 ACGCGCTGGAGCGGCTCTTCGCTGCTTCCTCCTCGGCGCAGCGGGGATGCCAGTTTCG 2891  
QY 242 AGGCGCGAAGCATGTACGAGCGCACACGCCCATCTGTGTCAAGGGGCGACG 289  
Db 2892 CCGTGCCTACGAGACAAGGACGCGGACCTCATGCTCGCGGCGGACG 2939

## RESULT 12

US-11-266-748A-57192  
; Sequence 57192, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 57192  
; LENGTH: 3487  
; TYPE: DNA  
; ORGANISM: Homo Sapiens

## US-11-266-748A-57192

Query Match 7.1%; Score 42.6; DB 8; Length 3487;  
Best Local Similarity 50.7%; Pred. No. 0.12;  
Matches 102; Conservative 0; Mismatches 99; Indels 0; Gaps 0;  
QY 1 GCGCTGCTGACAGCGCGCCACACAGACCGCGGAGCGGAGCGGATGCGGGCGC 60  
Db 379 GTGGTCCACCGCGCGCTGCGCGCGCGCGCGAGCTGTGTGTGGGGTTCGCGGCC 438  
QY 61 AGAAGCTGTTTGTATGACTCGGCGCGCGCAGAGGATGAAGCTGGCGTTGACACCTTC 120  
Db 439 GAGCTGGGCGGTGGGAGCGCGCGCTGCGCTGAGGCGCGCGCGCGCGCGCGG 498  
QY 121 TAGCATAAAGTGTGCTGCTGACCGGAGCTGTGCCCTTCTTCGAGTCCCTGGACATGCAA 180  
Db 499 GGGCAGCGGCGCTTGGCGCTGAGGAGCGGCGCTGTGGCTCGGGAGGTGGAGCTGGCG 558  
QY 181 GAGCAGAGATGAAGCAGGTC 201  
Db 559 GCGGAGGCGCGCGCAGGAC 579

## RESULT 13

US-10-449-902-7212  
; Sequence 7212, Application US/10449902

Publication No. US20060123505A1  
GENERAL INFORMATION:  
APPLICANT: National Institute of Agrobiological Sciences.  
APPLICANT: Bio-oriented Technology Research Advancement Institution.  
APPLICANT: The Institute of Physical and Chemical Research.  
APPLICANT: Foundation for Advancement of International Science.  
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
FILE REFERENCE: MOA-A0205Y1-US  
CURRENT APPLICATION NUMBER: US/10/449,902  
CURRENT FILING DATE: 2003-05-29  
PRIOR APPLICATION NUMBER: JP 2002-203269  
PRIOR FILING DATE: 2002-05-30  
PRIOR APPLICATION NUMBER: JP 2002-383870  
PRIOR FILING DATE: 2002-12-11  
NUMBER OF SEQ ID NOS: 56791  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7212  
LENGTH: 1467  
TYPE: DNA  
ORGANISM: Oryza sativa  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: AK064340  
DATABASE ENTRY DATE: 2001-12-06  
US-10-449-902-7212

Query Match  
Best Local Similarity 7.1%; Score 42.2; DB 6; Length 1467;  
Matches 80; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 285 CCACGGCTCGACACCGCCACTTTGACAGATCAAGCAGTACCTTGAGAGAGCGTGA 344  
DB 224 CTTGCTCCGAGTGGCGGACCTCGCGAGCGGTGGCGCTCCGAGATCTCCG 283  
QY 345 AGAGATGGGGCTCAAGCAGGATGTGATCCAGCAGCGCGGAGTGGTGGAGTCCACCG 404  
DB 284 CGAGATCGGCGGCAAGGTGCGCGAGATCCAGACAGGGCTCGGGAGACCGCTCCG 343  
QY 405 CGAGCAATTTGACTTNCCTCAACAA 428  
DB 344 CGACCTCAAGCAGCAGAGATCAACAA 367

RESULT 14  
US-10-449-902-15213  
Sequence 15213, Application US/10449902  
Publication No. US20060123505A1  
GENERAL INFORMATION:  
APPLICANT: National Institute of Agrobiological Sciences.  
APPLICANT: Bio-oriented Technology Research Advancement Institution.  
APPLICANT: The Institute of Physical and Chemical Research.  
APPLICANT: Foundation for Advancement of International Science.  
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
FILE REFERENCE: MOA-A0205Y1-US  
CURRENT APPLICATION NUMBER: US/10/449,902  
CURRENT FILING DATE: 2003-05-29  
PRIOR APPLICATION NUMBER: JP 2002-203269  
PRIOR FILING DATE: 2002-05-30  
PRIOR APPLICATION NUMBER: JP 2002-383870  
PRIOR FILING DATE: 2002-12-11  
NUMBER OF SEQ ID NOS: 56791  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15213  
LENGTH: 1052  
TYPE: DNA  
ORGANISM: Oryza sativa  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: AK065744  
DATABASE ENTRY DATE: 2001-12-06  
US-10-449-902-15213

Query Match  
Best Local Similarity 7.0%; Score 42; DB 6; Length 1052;  
Matches 90; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 162 CGAGTCCCTGGACATGCAAGAGCAGAGATGAAGCAGGTCAAGTTCATGAGCTTCGTGT 221  
DB 610 CAACTACTCACTACACACGCGGCTGATGAAGTGTCAAGTTCGCGGCTCGTCGG 669  
QY 222 TGGCGGAGCAGACCAATACAAAGGCGCGAAGCATGTAGAGCAGCAGCCCATCTGGTCAA 281  
DB 670 CTACGACAAACACGCTCTGGAACGCTCCGTGCTCCCGCGCAGCCGCCCATGCGCAA 729  
QY 282 GGCGCAGCGCTCGACACCGCCACTTTGACAAGATCAAGCAGTACCTTG 331  
DB 730 GTACATCCGCTACTACCGGACCTTGTGCTCGAGCTCAACAAGGCCCTCG 779

RESULT 15  
US-11-266-748A-3647/c  
Sequence 3647, Application US/11266748A  
Publication No. US20060134663A1  
GENERAL INFORMATION:  
APPLICANT: Harkin, Paul  
APPLICANT: Johnston, Patrick  
APPLICANT: Mulligan, Karl  
TITLE OF INVENTION: Transcriptome Microarray Technology and  
TITLE OF INVENTION: Methods of Using the Same  
FILE REFERENCE: 55815-0102 (319189)  
CURRENT APPLICATION NUMBER: US/11/266,748A  
CURRENT FILING DATE: 2005-11-03  
PRIOR APPLICATION NUMBER: EP 04105479.2  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105482.6  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105483.4  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105507.0  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105485.9  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105484.2  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: US 60/662,276  
PRIOR FILING DATE: 2005-03-14  
PRIOR APPLICATION NUMBER: US 60/700,293  
PRIOR FILING DATE: 2005-07-18  
NUMBER OF SEQ ID NOS: 483996  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 3647  
LENGTH: 575  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (530)..(530)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (543)..(543)  
OTHER INFORMATION: n is a, c, g, or t  
US-11-266-748A-3647

Query Match  
Best Local Similarity 7.0%; Score 41.6; DB 8; Length 575;  
Matches 89; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 266 ACGCCCATCTGGTCAAGGCGCCAGCGCTTGACCCGCGCACTTTGACAAGATCAAGCAGT 325  
DB 194 ACCTACTCTAGGCGCAGCGGCTTCTGCTGGCGCAGCTCACTTGAGCAGCGGCGAGT 135  
QY 326 ACCTTGGAGAGAGCGTGTCAAGAGATGGCGGTCAAGCAGGATGTGATCCAGCAGCGCCCG 385  
DB 134 CGGTGGCGGCAACCGCGCAGCAAGATCGGCTTCGGCATCTGCTCAGCAAGAGCGCCGACG 75  
QY 386 GAGTGTGAGTCCACCCCGGAGCAATTTGACTTNCCTCAACAACACTGGC 434

Db 74 GCGTGTGGGCGCTACAAACCGGGGAGACACCCCATCTTTCGTCAACTCCCC 26

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Job time : 187 secs



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 11, 2006, 10:30:14 ; Search time 5.5 Seconds

(without alignments)  
2855.090 Million cell updates/sec

Title: US-09-920-953-2

Perfect score: 1122

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 1301182

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA.\*

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5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pcp.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	232	20.7	126	2	US-09-920-540-13031
2	136	12.1	345	2	US-09-252-991A-32377
3	134.5	12.0	170	2	US-09-252-991A-19980
4	134	11.9	663	2	US-09-252-991A-30843
5	130.5	11.6	308	2	US-09-252-991A-27249
6	129	11.5	1476	2	US-09-252-991A-29427
7	126	11.2	235	2	US-09-252-991A-24046
8	125.5	11.2	394	2	US-09-252-991A-19344
9	124	11.1	312	2	US-09-252-991A-19787
10	122	10.9	726	2	US-09-252-991A-20675
11	121.5	10.8	204	2	US-09-252-991A-17837

#### ALIGNMENTS

##### RESULT 1

US-09-920-540-13031  
; Sequence 13031, Application US/09902540  
; Patent No. 6833447

; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; PRIOR FILING DATE: 2001-07-10

; PRIOR FILING DATE: 2001-07-10  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 13031  
; LENGTH: 126  
; TYPE: PRT

; ORGANISM: Myxococcus xanthus  
US-09-920-540-13031

Alignment Scores:  
Pred. No.: 3.63e-16

Score: 232.00  
Percent Similarity: 56.1%  
Best Local Similarity: 41.5%

Query Match: 20.7%  
DB: 2

Length: 126  
Matches: 51  
Conservative: 18  
Mismatch: 48  
Indels: 6  
Gaps: 2

US-09-920-953-2 (1-598) x US-09-920-540-13031 (1-126)

QY 37 ACGGCGGAAGCGGATGCGCGCGAGAGCTGTTTGTACCTGGCGCGCAGAGGC 96

Sequence 19787, A

Sequence 20675, A

DB 4 ThrAlaGlu-----LysSerValtyrGluGlnLeuGlyGluProAla 18

Sequence 18476, A  
Sequence 20161, A  
Sequence 20509, A  
Sequence 23215, A  
Sequence 24725, A  
Sequence 32478, A  
Sequence 32006, A  
Sequence 26487, A  
Sequence 26899, A  
Sequence 20771, A  
Sequence 20122, A  
Sequence 20433, A  
Sequence 30543, A  
Sequence 21783, A  
Sequence 25365, A  
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Sequence 30765, A  
Sequence 29217, A  
Sequence 20790, A  
Sequence 20172, A  
Sequence 19128, A  
Sequence 21837, A  
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Sequence 24828, A  
Sequence 16788, A  
Sequence 24634, A  
Sequence 31470, A  
Sequence 28232, A  
Sequence 24009, A  
Sequence 31760, A

US-09-252-991A-18476  
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US-09-252-991A-16788  
US-09-252-991A-24634  
US-09-252-991A-31470  
US-09-252-991A-28232  
US-09-252-991A-24009  
US-09-252-991A-31760

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Oy	97	ATGAAGCTGGCGTTGACACCTTCTACGATAAGGTGCTGCCTCACCCGAGCTGCTGCC	156
Db	19	MetAlaAlaValaGlulValPheYrArgLYsValLeuAlaAspHisSerHis	38
Oy	157	TTCATTGAGTCCCTGGACATGCAAGACGACAAGAAGATGAAGCAGGTCAAGTTTCATGAGCTTC	216
Db	39	PhePheGluAapValAaspMetGluArgGlnAlaAlaLysGlnLysAlaPheLeuThrMet	58
Oy	217	GTTGTTGGCGGAGCAGACCATAACAGGCCGGAAGCATGTACGCGCACAGCCCATCTGTG	276
Db	59	ValThrGlyGlyProValHisTyrSerGlyLYsAspMetArgAlaGlyHisAlaProLeu	78
Oy	277	GTCAAAGGCCACGGCTTGACACCACCCCATCTTGCACAGATCAACGAGTACTCTGGAGAG	336
Db	79	Vallys---ArgGlyIueuksnAspSerHisPheAspAlaValaAlaGlyHisLeuLYsAla	97
Oy	337	ACGCTGCAAGAGATGGGGGTCAAGCAGGATGTGTATCCAGCACGCGCCCGAGCTGGTAG	396
Db	98	ThrLeuGluGluLeuGlyValaAlaAlaProLeuValAlaArgValMetThrIleAlaGlu	117
Oy	397	TCCACCCGC	405
Db	118	SerAlaArq	120

## RESULT 2

US-09-252-991A-32377  
; Sequence 32377, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

Alignment Scores:	
Pred. No.:	8,97e-06
Score:	136.00
Percent Similarity:	34.8%
Best Local Similarity:	30.4%
Query Match:	12.1%
DB:	2
Length:	345
Matches:	70
Conservative:	10
Mismatches:	64
Indels:	86
Gaps:	10

US-09-920-953-2 (1-598) x US-09-252-991A-32377 (1-345)

Qy	539	CAGGCTCTCGGGCCCCCTGGCGCGCTCGGCAACTGGCGTCCCG	483
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Qy	482	TGGAATGACCGCTCAGGCTGGGTTGGGTTAATGAAATCAGTTGGGTGCGCAGTTGTTC	423
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Db	121	ProSerArgArgGln-	128
Qy	422	GGNAATCAAATTCGTCGGGTGGACTCCACCACTCGCGCGGTCTCGGA	371
		:::	
Db	129	GlnArgHisGlyLeuSerArgCysProLeu-ProLeuArgArgArgProSerProAla	148
Qy	370	-----TCACATCC	363
Db	148	atpArgGlnProProIleGluLeuGlyAlaValArgLeuArgProGlnArgArgPro	168

Qy	362	TGCTTGAGCCCATCTCTTGACGGTCTCTCCAAGTACTGCTTGATCTTGTCAAAGTGG	303
Db	168	oAlaGlnArgProAlaValAlaAla	176
Qy	302	CGGTGGT-----CCAGGCCGTGGCCCTTGACCATGGCGTGTGCGTCGTACATG	252
Db	177	GlyGlyGlnArgGlnProGlyArgAppProAlaGluHisLeuArgProArgArgPro--	195
Qy	251	CTTCGGCCCTTGATTTGGTCTGCTCCGGCCAAACACGAAGCTCATGAATTCGACCTGCTTC	192
Db	196	-----GlyLeuLeuArgArgProArgArg-----ProAlaG1	206
Qy	191	ATCTTCTGCTCTTCATGT-----CCAGGACTCGAAGAG	156
Db	206	nProGlyArgLeuAlaSerGlyArgGlyAlaGlyGlyAlaGluProGlySerArgArg	226
Qy	155	G-----GCAGCAGC	147
Db	226	gGlnValProGlyArgArgArgProPheArgSerProAlaGlyAlaAspArgAlaVal	246
Qy	146	TCGGGTCAGCCAGCACCTTATCTAGAGGTGTCAACCGCAGGTTCATGCGCTTCTGGG	87
Db	246	lProGlyGluProArgProGlyProArgArgArgProGluGlnArgProArgArgHi	266
Qy	86	CCGCCCAAGGTTCAT--CAACAGCTTCTTGCGCCGCATCCGCTTCGCGCGTCTCTG	30
Db	266	sArgProAlaHisGlyProGlyAlaGly-TyrProAlaAlaProLeuArgArgAlaGly	286
Qy	29	GTGCTGGTGGCCGGCTTCGACGGCAG	4
Db	286	lValAlaThrArgHisArgLeuArgGln	294

### RESULT 3

```

US/09-252-991A-19980
/ Patent No. 13980 Application US/09252991A
/ Patent No. 6551735
/ GENERAL INFORMATION:
/ APPLICANT: Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196_136

```

Alignment Scores:	9.92a-06	Length:	170
Pred. No.:	134.50	Matches:	68
Score:	38.3%	Conservative:	9
Percent Similarity:	38.3%	Mismatches:	45
Best Local Similarity:	38.3%	Indels:	79
Query Match:	12.0%	Gaps:	15
DB:	2		

US-09-920-953-2 (1-598) x US-09-252-991A-19980 (1-170)

QY	524	CTGGCGCGCTCGGCAACTGGCGCTCCCGCTCAA-----AATCGATGGAATGAGCGC	471
Db	14	ProGlyArgAsnArgAlaProAlaAlaAlaGlyArgArgSerAlaArg	33
QY	470	TCAGCTCG-----GGTGGGTTTAATGAAATCAGTTGGTGGCGAGTTGTTGGGNAAG	417
Db	34	SerGlyTTPProCysGlyTTP-----Arg-TTPSerHisProCysTTP-----	47
QY	416	TCAAAATCGTCGCGGTGGATCCACCACTCCGCGCGCGTGTGGATACATCCTGCTTG	357

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Db      48  GlnHisArgArgArgProArgProSerArgArg      ||| ||||| ||| ||||| ||| |||||
Qy      356 AGCCCATCTTTCAGCAGCTCTCTCAAGGTACTGCTGATCTGTCATAAGTGGGGTGG 297
Db      64  aArgPro      ||| ||||| ||| ||||| ||| |||||
Qy      296 TCAGGCGTGGCCCTTGACCAGAT-----GGCGGTGGCTGCTGCTACATGCTTCGG 246
Db      70  aAlaIleArgArgProValProAspGlyGlnProGlyArgArgArgAsnAlaCys----- 88
Qy      245 CCCTTGTATTGCTGCTCCCGCAACACGAAAGCTCATCAACTGACCTGCTTCATCTTC 186
Db      89  -----SerThrArg      ||| ||||| ||| ||||| ||| |||||
Qy      195 TGCTTTCATGTCAGGACTCGA-----AGAGGGCAGCAGC 147
Db      92  -----LeuProGlyArgArgArgPheProTrpArgProThrArgArgSerAl 108
Qy      146 TCCGGGTGAG-----CCAGCACCCTATCGTAGA-----AG 117
Db      108 aProGlySerArgThrGluArgAlaProSerProAlaArgArgGlySerArgArgSerAr 128
Qy      116 GTGTCAACCGCAGCTTCATGCTCTCTCGCGCCAGGTCAACACAGCTTCTTGGC 57
Db      128 gArgArgProAlaAla-----ArgArgGlyThrLeuProCysProAlaCysE 144
Qy      56  CCGATCCCGCTTCGC-----CGTCTCT-----GGTCTGCTGGCGCGCTCTGC 10
Db      144 r-AlaSerArgAsnArgSerArgSerCysArgSerGlySerAlaGlyArgSerCys 163

```

## RESULT 4

```

US-09-252-991A-30843
; Sequence 30843, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30843
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30843

```

```

Alignment Scores:
Pred. No.: 1.87e-05 Length: 663
Score: 134.00 Matches: 53
Percent Similarity: 35.7% Conservative: 17
Best Local Similarity: 27.0% Mismatches: 71
Query Match: 11.9% Indels: 55
DB: 2 Gaps: 13

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US-09-920-953-2 (1-598) x US-09-252-991A-30843 (1-663)

```

```

Qy      512 CGCAACTGGCTCCCGCTCAAAATCGATGG-----AAT 477
Db      45  ArgArgValProIleArgCysAlaAsnAlaTrpProGlyArgProMetSerSerThrSer 64
Qy      476 GAGCGCTCAGCTGGGGT-----TGGGTTATGAAAT 444
Db      65  ArgArgProGlyTrpSerProAlaValProAlaGlyAlaCysCysTrpLysThrArgAsn 84
Qy      443 CAGTTGGTGGCAGTTGTTGGGNAAGTCAAATTCGTCGGGGTGGACTCCACCCTCCG 384

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Db      85  ValAlaGlyArgSerAlaThrAspAlaTrpSerSer-----AlaProAlaPro 100
Qy      383 CGCGCTGCTGGATCACAATCTGTTGACGGCCATCTCT-----TGCAGCGTCTCT 333
Db      101 AlaAsnCys-----CysCysLeuPheProAlaGlyProSerProAlaSerProAla 117
Qy      332 CCAAGGTACTGCTTGAATCTTCTCAAGTGGCGGTGGTCCAGGCCG-----TGGCCC 282
Db      118 ProAlaAlaCysArg-----ArgTrpProArgAlaAlaCysHisTrpPro 132
Qy      281 TTGACCAAGTGGCGTGGCTGCTGCTACATGCTTCCGGCC-----TTGATTGCTCTCT 228
Db      133 AlaSerAlaTrp-----TrpTrpLeuAlaProAlaArgCysCysTrpProAla 148
Qy      227 CCGCAACACAGAACTCATGAACCTTGACCTGCTTCTCTGCTCTTGCATGCTCCAGG 168
Db      149 ProPro-Ala-----ProAlaSerAlaGlyArgAlaCysCysAlaSe 162
Qy      167 GACTCGAAGAGGCAGCAGCTCCGGGTCCAGCAGCAGCCTTATCGTAGAAGGTGTCAACC 108
Db      162 rProAsnArgArgArgGluProTrpProProSerProTrpAlaSerArgAla---G1 181
Qy      107 GCCAGCTTTCATGCTTCTGCGCCGCCAGGTCAACACAGCTTCTTCCGCCCGCATCCC 48
Db      181 yProAlaSerCys-----GlyArgPro-----ProAlaCysSerProValAl 195
Qy      47  GCTTCCCGCTCTCTGCTGCTGGTGGCGCGCTGCTGCAGGACGCG 2
Db      195 aThrAlaProThrAlaThrCysSerProProSerProAlaArgSerAla 210

```

## RESULT 5

```

US-09-252-991A-27249
; Sequence 27249, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27249
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27249

```

```

Alignment Scores:
Pred. No.: 3.31e-05 Length: 308
Score: 130.50 Matches: 77
Percent Similarity: 36.6% Conservative: 13
Best Local Similarity: 31.3% Mismatches: 81
Query Match: 11.6% Indels: 75
DB: 2 Gaps: 17

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US-09-920-953-2 (1-598) x US-09-252-991A-27249 (1-308)

```

```

Qy      593 GGTGCGAAAATGGCTGATGGCTTCAATGCAGCAGAGGCTGCACAAAGATTTCAGGCT 534
Db      21  GlyAlaGlyProGlyArgGlyGlySer---GlyProGlyArgAlaGlyArgArgSerIle 39
Qy      533 CTGGGCGCCCTGGCGCGCTCGGCAACTGGCGCTCCCGCTCAAAATCGATGGAATGAG 474
Db      40  ProProAlaProArgArgGlyProArgLeuAlaArgProSerArgGlyArgGlyArgThr 59
Qy      473 CGC-----TCAGCTGGGGTGGGT-----AATGAAATCAGTTG 438
Db      60  ArgAlaProGlyArgCysCysSerGlyTrp---TrpSerThrGlySer-ProMetAlaPr 78

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Qy	437	GGTGGCGAGTTGTTGGGNAAGTCAAATTGGT-----CGCGGTGGACTCCACCACCTCGG	384
Db	78	oValArgSerAlaCysArgGlyThrSerArgProValArgSerTrpProGlyProProAla	98
Qy	383	CGCGGTCTCGATGCACATCTCGTTTGACGC-----CCATCTCTTGC	342
Db	98	aGlyArgAlaGlyGlyTyrGlyArgArgGlyProArgArgSerValProProThrVa	118
Qy	341	AGCGTCTCTCCAAGGTACTGTTTGAATCT-----TGTCAAAGTGGCGGTGGTCC	294
Db	118	lAlaSerValAlaGlyProSerArgSerGlyAlaGlyProAlaArgAlaAlaGlyPr	138
Qy	293	AGCGGTGGCCCTTGACCA-----	275
Db	138	oGlyAlaAlaProCysProGlyProGlyArgGlySerGlyAlaAlaArgArgHisArgAr	158
Qy	274	-----CATGGCGTGTGCGTCGTACATGCTTCGGCCCTTGTATTGGTCTCTGCTCGG	225
Db	158	gGlyArgArgProGlyArgArgSerArgTrpCys-----ProCysAlaGly---SerAr	175
Qy	224	CAAACACGAAGCTCATGAACCTTGACCTTCATCTTCTGCTCTTGCATGTCACAGGAC	165
Db	175	gAlaArgArgProSer-----GlyCysThrGlyCys	185
Qy	164	TCGA-----AGAAGGCCA-----GCAGTCCGGTTCAGCCAGCACCTTA	126
Db	185	sArgProArgLeuProArgArgAlaGlyArgArgAlaAlaGlyGlyArgProPro-----	203
Qy	125	TCGTAGAAGGTGTCAACCGCCAGCTTTCATGCTTCTGCGCGCCCGCCAGGTTCATCAA-----	71
Db	204	-----CysCysProProGlyAla-----ProGlyGluArgGlySerAr	215
Qy	70	-----ACAGTTCCTTCGCGCCGCATCCCGCTTCGCGCGTCTCTGTGGTCTGGTGC	15
Db	215	gSerThrGluSerSerAlaArg---ProAlaProArgProCysGlyGlySerGlyArgG	234
Qy	14	TCTGCAGGCAGCGC	1
Db	234	lyAlaArgHisArg	238

RESULT 6  
US-09-252-991A-29427  
; Sequence 29427, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

Alignment Scores:		
Pred. No.:	8.64e-05	1476
Score:	129.00	74
Percent Similarity:	33.5%	10
Best Local Similarity:	38.0%	Conservative:
Query Match:	11.5%	Mismatches:
DB:	2	Indels:
		Gaps:

US-09-920-953-2 (1-598) x US-09-252-991A-29427 (1-1476)

[illegible]

RESULT 7  
US-09-252-991A-24046  
; Sequence 24046, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142

Alignment Scores:		
Pred. No.:	9, 02a-05	235
Score:	126.00	47
Percent Similarity:	39.2%	18
Best Local Similarity:	28.3%	58
Query Match:	11.2%	15
DB:	2	10
	Length:	
	Matches:	
	Conservative:	
	Mismatches:	
	Indels:	
	Gaps:	

```

US-09-920-953-2 (1-598) x US-09-252-991A-24046 (1-235)
QY 482 TGGATGAGCGCTCAGGC---TGG-----GGTTGGTTAATAAATCAG 441
Db 26 TrpAspGlyArgSerGlyArgTrpSerArgArgTrpCysAlaTrp----- 40
QY 440 TTGGGTGCGCAGCTTGTGGNAAGCAAAATTCGTCCGGGTGAGCTCCACCACTCCGGCG 381
Db 41 ---GlyCysProSerValAlaProThrArgTrpSerArgGlyCysSerArgSerProPro 59
QY 380 GCGTCTGGATCACAATCTCTGTGTGACGCCCACTCTTGCAGCGCTCTCCCAAGGTACTGC 321
Db 60 CysAlaTrpAlaSerSerAlaIleThrProTrpProArgThrArgSerProSer----- 77
QY 320 TTGATCTTGTCAAGTGGGGTGTCCAGGCGGTGACCGCTTGACAGATGGCGGTGTCG 261
Db 78 -----ArgArgTyThrTrp---ArgSerTrp-----CysArgTrpGlyCysArg 91
QY 260 TCGTACATGCTCGGCCCTTGTATTGGTCTGCTCGCCCAAAACACCAAGCTCATGACTTG 201
Db 92 -----ThrProProPro---Thr----- 96
QY 200 ACTGCTTCATCTTCTGTCTGTGATGTCAGGGACTCGAAGAGGGCAGCAGCTCCGGG 141
Db 97 -----AlaSerAlaSerIleSerAlaProAlaAlaCysSerIleHisAlaAlaProGl 114
QY 140 TCAGCCAGCAGCTTATCCTAGAGTGT-----CAAGCGCAGCAGCTTCATGCGCT 93
Db 114 yValSerAlaSerAlaSerAlaAlaArgCysAlaCysSerSerProGlySerSerGlyGl 134
QY 92 TCTGCGCGCCAGGTCAATCAACAGCTTCTTGGCGCGCATCCGCTTCCGCGTCTCT 33
Db 134 yCysArgArgProSerSerAlaCysSerSerThrAla---ThrProArgProThrGlyAr 153
QY 32 GTGGTCTGTGGCGCG 17
Db 153 gTipProArgTrpPro 158

RESULT 8
US-09-252-991A-19344
; Sequence 19344, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19344
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19344

Alignment Scores:
Pred. No.: 0.000124 Length: 394
Score: 125.50 Matches: 68
Percent Similarity: 31.8% Conservative: 16
Best Local Similarity: 25.8% Mismatches: 76
Query Match: 11.2% Indels: 104
DB: 2 Gaps: 11

US-09-920-953-2 (1-598) x US-09-252-991A-19344 (1-394)
QY 17 CGGCCACGACCCACAGAGACGG-----CGG 43

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Db 116 ArgProGlyAlaProGluProArgGlyThrProProValGlyProGlySerLeuSerArg 135
QY 44 AAGCGGATCGCGCGCAAGAAGCTGTTGATGACCTGGCGG-----CGCAG 91
Db 136 ArgIysProAlaGly-AspLeuAla-----ProProArgGlnLeuAlaAspArgPr 152
QY 92 AAGCATGAAGCTCGCGGTTGACACCTTCTACGATAAGTGTCTGCTGACCGGAGCTGC 151
Db 152 oAlaHisProProGlyGlySerHisLeuGlnLeuProGlyAlaGlyProProGlyArgVa 172
QY 152 T-----GCCCTTCTTCGA----- 164
Db 172 lArgProAlaValSerLeuProProAlaValPheArgArgLeuHisGlnProAlaValAr 192
QY 165 -----GTCCCTGGACATCAAGAGCAGCAAGATGAAGCAGGTCAAGTTTCATGAGTTCG 217
Db 192 gArgProLeuProGlyHisAlaAla-----AlaGlyArgThrHisProGlnAl 209
QY 218 TGT-----TGGCGGAGCAGACCAT 238
Db 209 aValProProAlaLeuSerArgArgProAlaGlyAlaProGlyArgArgGlnProAs 229
QY 239 ACA-----GGCGCGAAGCATGTACGACGACACGCGCCATCTGTCACAGGCGCCAGCTCGG 295
Db 229 pGlnProAspProProAlaArgProArgLeuProAlaLeuAlaGlyProArgProGl 249
QY 296 ACCACGCCACTTTGACAGATCAAGCAGTACCTTTGGAGAGAGCTGCAAGAGATGGCG 355
Db 249 yArgProProThrAlaHisGluPheAlaAspProAlaThrProProAlaArgGlyArgAr 269
QY 356 TCAA----- 359
Db 269 gGlnLeuProAlaThrGlnGlyProProAlaAlaArgProGlyAspLeuProProGlySe 289
QY 360 ---GAGGATGTATCCAGCAGCGCGCGAGTGTGGAGTC----- 398
Db 289 rGlyArgAlaValAspProGlyHisArgArgAlaAlaArgLeuPheArgAlaLeuGlyLe 309
QY 399 -----CACCGCGAGCAATTTGACTTNCCTCAACA 427
Db 309 uProSerArgValGlnGluValAspArgProHisProArgVal----- 324
QY 428 ACTGCGCACCACTGATTTTCAACCAACCCAGCCTGAGCGCTCATTCCATCGAT 487
Db 325 -----ProAlaProGlyGlySerLeuLysLeuSerPr 335
QY 488 TTTGAGCGGGAGCGCAGTGTGCGAGCGCGCCAGCGGCGCCAGGAGCTGCAAAATCGT 547
Db 335 oThrProGlyAspGluAlaArgCysAlaValGlyArgAlaProTrpArgThrAlaAlaAl 355
QY 548 TTGCCAGGCC 557
Db 355 aAlaArgPro 358

RESULT 9
US-09-252-991A-19787
; Sequence 19787, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19787
; LENGTH: 312
; TYPE: PRT

```



; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 17837  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-17837

Alignment Scores:  
Pred. No.: 0.000258 Length: 204  
Score: 121.50 Matches: 60  
Percent Similarity: 34.6% Conservative: 15  
Best Local Similarity: 27.6% Mismatches: 77  
Query Match: 10.8% Indels: 65  
DB: 2 Gaps: 14

US-09-920-953-2 (1-598) x US-09-252-991A-17837 (1-204)

```
QY 5 TGCTGCAGACGGCGCCACACGACGACGAGCGGCGGAGCGGATCGGGCGCAAGA 64
Db 7 CysSerSerThrArgProThrProThrTrp-----ProSerAlaAsn 21
QY 65 AGCTGTTGATGACCTGGCGGCGGCGAGAGGATGAAGTGGCGTTGACACCTTCTACG 124
Db 22 SerMetAlaThrAlaTrpProPheProAlaAlaSerTrpArgThr-----Thr 39
QY 125 ATAAGTGTGG-----CTGACCGGAGTGC-----151
Db 40 SerArgCysAlaProAlaThrAspArgSerCysSerThrAlaThrSerGlyIleArg 59
QY 152 TGCCCTTCTCGAGTCCCTGGACATCAAGACGACGAGATGAAGCAGGTCAAGTTCATGA 211
Db 60 CysGlyThrSerArgProTrp---AlaGlySerArgProProArgSerSer-----76
QY 212 GCTTCGTGTTGGCGGACGACCAATACAAAGGCGCGAAGCATGTACGACGACACGCC 271
Db 77 -----ArgGluProGluProCys-----ArgAlaPro 85
QY 272 ATCTGTCAAGGCCACGGCTGGACACCGCCACTTTGACAGATCAAGCAGTACTTGG 331
Db 86 ProTrpSer-----AlaAlaTrp-----AlaAlaThrCys 95
QY 332 GAGACGCTGCAAGAGATGGCGTCAAGCAGGATGTGATCCAGCAGCGCGCGGAGTGG 391
Db 96 ProArgProCysSerAlaThrThrCysSer-----ProProSerTrp 109
QY 392 TGGAGTCCACCGCGAGATTTGACTTNCACCAACTGCGCACCCCACTGATTTTCAT 451
Db 110 ThrLeuProThrProGlySerAlaAlaAlaProAlaCysAlaSerGlyIle-----126
QY 452 TAACCAACCCAGCTGACGCTCATTCATGATTTTGGCGGGGAGCGCCAGT---508
Db 127 -----SerProAlaThrSerAla---AlaAlaThrTrpProCysGlyArgProPro 143
QY 509 -----GCCGAGCGCGCGCGGCGCCAGGAGCGCTGCAAAATCGT 547
Db 144 ArgSerProArgGlyTrpSerGluSerMetArgTrpCysTrpGlnProAla-----161
QY 548 TTCCCGACCCCTGCTGATTAAGAGGACCATCAGCCATTTTCGACCAAGCC 598
Db 162 ---ProAlaThrSerAlaAlaArgProProArgProGlySerArgArgAla 177
```

RESULT 12

US-09-252-991A-18476  
; Sequence 18476, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 18476  
; LENGTH: 351  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18476

Alignment Scores:  
Pred. No.: 0.000317 Length: 351  
Score: 121.50 Matches: 58  
Percent Similarity: 33.5% Conservative: 10  
Best Local Similarity: 28.6% Mismatches: 58  
Query Match: 10.8% Indels: 77  
DB: 2 Gaps: 10

US-09-920-953-2 (1-598) x US-09-252-991A-18476 (1-351)

```
QY 30 CACAGACGGCGGAGCGGATCGGCGGCGCAAGAGCTGTTGATGACCTGGCGGCGC 89
Db 131 HisArgAlaAlaGlyArgGlyProAlaAlaGlyProSerGlyProArgProGlyArg 150
QY 90 AGA-----AGGCATGAAGTGGCGGTTGACACCTTCTACGATAAGGT 131
Db 151 LysProAlaValArgProAlaArgHisAlaAlaProAla-----163
QY 132 GCTGCTGACCGGAGCTGCTGCCCTTCTCGAGTCCCTGGA-----CATGCA 179
Db 164 -----ProGlyLysAspProArgArgArgGlyAspGlnGluProHisArg 180
QY 180 AGACGAGAAGATGAACGAGGTCAAGTTCATGAGCTTCGTGTTGGCGGAGCAGCAATA 239
Db 181 AlaAlaArgArgAlaGlyGlyAlaHis-----ArgProTrpArg---ArgProLeu 197
QY 240 CAAGGCGCGAAGCATGTACGACGACACGCCCATCTGTCAAAGGCGCGCTGGACCA 299
Db 198 ProGlyProAspHisProArgGlyGlnProAlaGlyGlyIleProHisAla-----215
QY 300 CGCCACTTTGACAAGATCAAGCATGACCTTGGAGAGACGCTGCAAGAGATGGCGTCAA 359
Db 216 -----AlaIleArgArgGlyArgGln 222
QY 360 -----GCAGGATGTATCCAGCA-----CGCCGCGCG 386
Db 223 AlaLeuArgAlaGlyArgGlnProAlaProAspArgProLeuHisArgArgArgArg 242
QY 387 AGTGTGGAGTCCACCGCGCAGCAATTTGACTTNCACCAACTGCGCGCCCACTGATT 446
Db 243 ProGlyAlaValAlaProAlaArgLeuGlyAsnLeuAlaGlyGlnAlaGln-----260
QY 447 TTCAATTAACCCCAACCCCGCTGAGCGCTCATTCATCGATTTTGGAGCGGGAGCGCCAG 506
Db 261 -----GlyArgArgAla 264
QY 507 TTGCGC-----AGCGCGCCAGGGGGCGCCAGGAGC 536
Db 265 GlyProArgArgArgArgAlaAlaArgHisLeuArgProProArgArgProArgArg 284
QY 537 CTGCAATC 545
Db 285 LeuArgVal 287
```

RESULT 13

US-09-252-991A-20161  
; Sequence 20161, Application US/09252991A

Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 20161  
LENGTH: 248  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20161

Alignment Scores:  
Pred. No.: 0.000314 Length: 248  
Score: 121.00 Matches: 47  
Percent Similarity: 35.1% Conservative: 19  
Best Local Similarity: 25.0% Mismatches: 62  
Query Match: 10.8% Indels: 60  
DB: 2 Gaps: 11

US-09-920-953-2 (1-598) x US-09-252-991A-20161 (1-248)

QY 2 CGCTGCTGCAGACGGCCACACGACGCGGAGCGGATCGGGC 58  
DB 56 ARGCSyAlaArgSerProProAlaGlyProSerSerThrArgArgProAlaSer 75  
QY 59 GCAAGA---AGTGTGTGATGACCTGGCGCGGACGAGCATGAGCTGGCGGTGACA 115  
DB 76 AlaSerIleArgCys-----SerAlaArgValArgIleTrpSerThr 90  
QY 116 CTTCTACATAGG----- 130  
DB 91 SerAlaThrIleArgLysAsnSerAlaAlaAsnThrLysAlaAlaArgTrpCysArg 110  
QY 131 ---TGCTGGCTGACCGGAGC-----TGCTGC----- 154  
DB 111 ARGCSyAlaCysTrp---ThrArgAsnArgProAlaArgSerCysArgCysValAla 129  
QY 155 -----CCTTCTCGAGTCCCTGGACATGC 178  
DB 130 ThrArgSerSerAlaProProThrProProAlaProThrSerIleProThrProCys 149  
QY 179 AAGACGAGATGAGCAGGTCAAGTTCATGCTGCTGTTGGCGGACGACCAAT 238  
DB 150 ThrArg-----AlaThrCysAlaAlaSerAlaAla--- 159  
QY 239 ACAAGCGCGGAGCATGTACGACGACACGCGCATCTGGTCAAGCGCCAGCGCTGGACC 298  
DB 160 ThrArgGlyArgSerCysAlaThr---ThrLysArgTrpArgSerAlaGlySerThrAla 178  
QY 299 ACCGCCACTTTCACAAAGTCAAGCAGTACCTTTGGAGAGACGCTGCAAGAGATGGCGTCA 358  
DB 179 ProGlyLysSerAlaAlaThrProAlaThrThrAlaArgArgCys-----TrpSerThr 196  
QY 359 AGCAGATGTGATCCAGACGCGCGGAGTGGTGGATCCACCGCGCAAGATTGGACT 418  
DB 197 ProGlnAlaProGlyAlaThrProSerProGlyTrpProAlaSerAlaArgTrpAlaCys 216  
QY 419 TNCCCAACAACCTGCCACCCCACT 442  
DB 217 SerProSerAlaAlaGlnProSer 224

RESULT 14  
US-09-252-991A-20509  
Sequence 20509, Application US/09252991A  
Patent No. 6551795

GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 20509  
LENGTH: 686  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20509

Alignment Scores:  
Pred. No.: 0.000461 Length: 686  
Score: 121.00 Matches: 51  
Percent Similarity: 35.2% Conservative: 5  
Best Local Similarity: 32.1% Mismatches: 47  
Query Match: 10.8% Indels: 56  
DB: 2 Gaps: 9

US-09-920-953-2 (1-598) x US-09-252-991A-20509 (1-686)

QY 3 GCTGCTGCAGACGGCCACACGACGCGGAGCGGATCGGGCGCAA 62  
DB 117 AlalaCysArgArgGlyAlaTrpHis-----GlyLeuArgProArg 130  
QY 63 GAAGCTGTTTGCATGACCTGGCGCGGACGAGCATGAGCTGGCGGTGACACCTTCTA 122  
DB 131 ProAla-----GlyArgArgArgProAlaAlaGlyGly- 142  
QY 123 CGATAAGGTGCTGCTGACCGGAGCTGCTGCCCTTCTTCGAGTCCCTGGACATCGCAAGA 182  
DB 143 -----GlnArgTyrAlaAlaGluArgCysAlaGlyLeuAlaArg 155  
QY 183 GCAGAAGATGAAGCAGGTCAAGTTCATGAGCTTCTGTTTGG----- 224  
DB 156 ProAlaProArgThr-----ValAlaArgArgArgProTrpArgHisProArgCysAla 173  
QY 225 -----CGAGCAGACCAATACAAAGCGCGGAGCATGTACGACGACACGCCCATCTGCT 278  
DB 174 ValProArgGlyArgProAlaAlaGlyAla-----AlaAlaArgArgGlyAlaGly 191  
QY 279 CAAGGCGCACGGCTGGACCCACCGCCACTTTGCAAGATCAAGCAGTACCTTGGAGAC 338  
DB 192 GlyGlyIleGlnProGlyLeuPro-----CysLeuAlaTrpArgAla 205  
QY 339 GCTGCAAGA-----GATGGCGGTCAA 359  
DB 206 AlalaArgGlyLeuAlaArgLeuProProGlyGlnProTrpAlaThrGlyAlaArgGln 225  
QY 360 GCAGATGTGATCCAGACGCGCGCGGAGTGGTGA-----GTCCACCCG 404  
DB 226 ProGlyAlaGlyAlaGlyProArgArgGlyGlyGlyValaArgArgThrHisPro 244

RESULT 15  
US-09-252-991A-23215  
Sequence 23215, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18



; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 23215  
; LENGTH: 219  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-23215

## Alignment Scores:

Pred. No.:	0.000383	Length:	219
Score:	120.00	Matches:	57
Percent Similarity:	38.1%	Conservative:	18
Best Local Similarity:	29.1%	Mismatches:	72
Query Match:	10.7%	Indels:	49
DB:	2	Gaps:	9

US-09-920-953-2 (1-598) x US-09-252-991A-23215 (1-219)

Qy	593	GGTGGGAAATGGCTGATGGCTTCAATGACGAGGGCTGGCAACGATTTCAGGCT	534
Db	58	GlyArgArgTyrSerAspArgSerAlaPro-----AlaAsnProProGly	73
Qy	533	CCTGGGCCCCCTGGCGGCTGCGCAACTGCGCTCCOC-----GCTCAAAATCGA	483
Db	74	ProGlySerValProArgSerArgArgTyrAlaValProGlyAlaAlaArgSerArg	93
Qy	482	TGGAATGAGCGCTCAG-----GCTGGGTTGGGTTAATGAAATCAGTTGGGT	435
Db	94	-ProAlaThrGlyProProArgTyrAlaGlyProGlyHisArgAlaAlaAlaTyrLe	113
Qy	434	GCGCAGTTGTTGGGNAAGTCAAATTCGTCGGGGTGGACTCCACCACTCCGGCGCGTGC	375
Db	113	uArg-----ArgArgAlaSe	118
Qy	374	TGGATCACATCTGTTGACGCCCATCTCTTGACGGCTCTCCAAAGTACTGCTTGATC	315
Db	118	rAlaSerCysProGlyHisArgArgGlyAspSerGlySerProGlyProArgLysAl	138
Qy	314	TTGTCAAAGTGGCGGT-----GGTCAGGCGGCTGGCCCTTGACCAGATGGCGGTGT	264
Db	138	aThrArgGlyHisGlyArgLysArgProProGlyArg-----ProAspAlaProva	155
Qy	263	GCGTCGTACATGCTTCGGCCCTTGTATTGGTCTGCTCCGCCAAACACAGCACTCATGAAC	204
Db	155	lArgArg-----AlaProAlaAsnSerVal-----	163
Qy	203	TTGACCTGCTTCATCTTCTGCTCTTGCAATGTCAGGGACTCGAAGAGGGCAGCGCTCC	144
Db	164	-----ProAlaSerArgGlyArgAlaGlyCysSerArgPheArgCysArgThrProAlaPr	182
Qy	143	GGGTGAGCCAGCACCTTATCTAGAAAGGTGTCAACCGCCAGCTTCATCGCTTCTGCGCCG	84
Db	182	oGlyAlaProAlaArgProAlaGlyArgArgSerProProAlaArgCys-----Ar	199
Qy	83	CCCAGTTCATCAACAGCTTCTTGGCCCGCATCCGCTTCGCGCG	38
Db	199	gSerGlyCysAlaAlaAlaArgGlyProProValProValProPro	214

Search completed: August 11, 2006, 10:31:40  
Job time : 33.5 secs

GenCore version 5.1.9  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 11, 2006, 10:30:49 ; Search time 20.8 Seconds  
(without alignments)  
3995.228 Million cell updates/sec

Title: US-09-920-953-2

Perfect score: 1122

Sequence: 1 gcgcgtcgcagcgcggc.....agccatttttcgaccacagcc 598

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 4195594

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/abs/ABSSWEB.spool/US0920953/runat\_10082006\_163819\_5480/app\_query.fasta\_1  
-DB=Published Applications AA.Main -QFMT=fastan -SUFFIX=rapbm -MINMATCH=0.1  
-LOPCCI=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cgi -LIST=45 -DLOCALIGN=200 -THR\_SCORE=pcr -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abs02p  
-USER=US0920953 @CNC 1 1 342 @runat\_10082006\_163819\_5480 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOC=100 -LONGLOG -DEV TIMEOUT=120  
-WAEN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA.Main:

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3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	254.5	22.7	124	4	US-10-282-122A-61519
2	148	13.2	324	4	US-10-425-114-58160
3	148	13.2	428	6	US-11-096-568A-19503
4	148	13.2	544	6	US-11-096-568A-19501
5	142.5	12.7	19723	4	US-10-084-846A-5
6	138.5	12.3	212	6	US-11-096-568A-22256
7	128	11.4	210	6	US-11-096-568A-8162
8	125	11.1	417	4	US-10-437-963-143835
9	125	11.1	19695	4	US-10-084-846A-3
10	124.5	11.1	19662	4	US-10-084-846A-6
11	120.5	10.7	19608	4	US-10-084-846A-8

12	120	10.7	375	6	US-11-096-568A-23618	Sequence 23618, A
13	119.5	10.7	276	4	US-10-437-963-166380	Sequence 166380, A
14	117.5	10.5	309	6	US-11-096-568A-18960	Sequence 18960, A
15	117.5	10.5	384	4	US-10-425-114-72136	Sequence 72136, A
16	117.5	10.5	384	4	US-10-425-114-72137	Sequence 72137, A
17	117.5	10.5	19723	4	US-10-084-846A-5	Sequence 5, Appli
18	117	10.4	325	6	US-11-096-568A-24112	Sequence 24112, A
19	117	10.4	369	6	US-11-096-568A-24111	Sequence 24111, A
20	117	10.4	373	6	US-11-096-568A-24110	Sequence 24110, A
21	116.5	10.4	19652	4	US-10-084-846A-7	Sequence 7, Appli
22	115.5	10.3	155	4	US-10-437-963-103601	Sequence 103601, A
23	115.5	10.3	224	4	US-10-437-963-141171	Sequence 141171, A
24	115.5	10.3	517	4	US-10-425-114-63797	Sequence 63797, A
25	115.5	10.3	517	4	US-10-425-114-63798	Sequence 63798, A
26	115.5	10.3	517	4	US-10-425-114-63800	Sequence 63800, A
27	115.5	10.3	728	4	US-10-425-114-63691	Sequence 63691, A
28	115	10.2	274	4	US-10-425-115-293205	Sequence 293205, A
29	114.5	10.2	381	4	US-10-425-114-47573	Sequence 47573, A
30	114.5	10.2	401	4	US-10-425-114-40384	Sequence 40384, A
31	114.5	10.2	599	5	US-10-450-763-33889	Sequence 33889, A
32	113.5	10.1	398	4	US-11-096-568A-21570	Sequence 21570, A
33	112.5	10.0	352	6	US-11-096-568A-21569	Sequence 21569, A
34	112.5	10.0	355	6	US-11-096-568A-25691	Sequence 25691, A
35	112	10.0	199	6	US-10-425-114-48205	Sequence 48205, A
36	112	10.0	247	4	US-10-084-846A-4	Sequence 4, Appli
37	112	10.0	19725	4	US-10-437-963-176482	Sequence 176482, A
38	111	9.9	265	4	US-11-096-568A-22088	Sequence 22088, A
39	111	9.8	424	6	US-10-437-963-106950	Sequence 106950, A
40	110.5	9.8	294	4	US-11-096-568A-12965	Sequence 12965, A
41	110.5	9.8	464	6	US-10-425-114-65735	Sequence 65735, A
42	110.5	9.8	492	4	US-10-370-7158-636	Sequence 636, App
43	110	9.8	249	5	US-11-096-568A-22088	Sequence 22088, A
44	109.5	9.8	424	6	US-10-425-114-66510	Sequence 66510, A
45	109.5	9.8	530	4		

#### ALIGNMENTS

#### RESULT 1

US-10-282-122A-61519  
Sequence 61519, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Orlsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamanoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27

;; PRIOR APPLICATION NUMBER: 60/257,931  
;; PRIOR FILING DATE: 2000-12-22  
;; PRIOR APPLICATION NUMBER: 60/267,636  
;; PRIOR FILING DATE: 2001-02-09  
;; PRIOR APPLICATION NUMBER: 60/269,308  
;; PRIOR FILING DATE: 2001-02-16  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 78614  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 61519  
;; LENGTH: 124  
;; TYPE: PRT  
;; ORGANISM: Legionella pneumophila  
US-10-282-122A-61519

Alignment Scores:  
Pred. No.: 1,01e-15 Length: 124  
Score: 254.50 Matches: 49  
Percent Similarity: 64.1% Conservative: 26  
Best Local Similarity: 41.9% Mismatches: 41  
Query Match: 22.7% Indels: 1  
DB: 4 Gaps: 1

US-09-920-953-2 (1-598) x US-10-282-122A-61519 (1-124)

QY 61 AAGAGCTGTTGATGACCTGGCGCGCCAGAGCATGAGCTGGCGGTTGACACCTTC 120  
DB 3 GluSerLeuPheGluArgLeuGlyGlyGlnAsnAlaValAsnThrAlaValAspPhe 22  
QY 121 TACGATGAAGTGTGGCTGACCGCGGAGCTGCTGCCCTCTTCGAGTCCCTGGACATCAA 180  
DB 23 TyrArgLysMetLeuMetAspAspArgValAsnTyrPhePheAspValAspMetGlu 42  
QY 181 GAGCAGAGATGAAGCAGGTCAAGTTCATGAGCTTCGTTGCGGAGCAGACCAATAC 240  
DB 43 GlnGlnLeuLysGlnLysGlyPheLeuThrMetValPheGlyGlyProAsnGlnTyr 62  
QY 241 AAGGCCGAGCATGTACGACCGCACGCCCATCTGTCTCAAGGCCACGGCTGAGCAC 300  
DB 63 ThrGlyLysSerMetArgGlyGlyHisLeuLeu---AlaArgGlyLeuAsnAsp 81  
QY 301 CGCCACTTTCACAGATCAAGCAGTACTTGGAGAGAGCGCTGCAAGAGATGGCGTCAAG 360  
DB 82 SerHisValAspIleValIleGluHisLeuGlyGluThrLeuLysGluLeuGlyAlaAsn 101  
QY 361 CAGATGTGATCCAGCAGCGCGCGGAGTGTGGAGTCCACCCCGCAGCAA 411  
DB 102 GluGluAspIleGlnLysValAlaAlaIleAlaAsnSerValArgGlyAsp 118

## RESULT 2

US-10-425-114-58160  
;; Sequence 58160, Application US/10425114  
;; Publication No. US2004003488A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Liu, Jingdong  
;; APPLICANT: Zhou, Yihua  
;; APPLICANT: Kovalic, David K.  
;; APPLICANT: Screen, Steven E  
;; APPLICANT: Tabaska, Jack E  
;; APPLICANT: Cao, Yongwei

;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
;; FILE REFERENCE: 38-21(5313)B  
;; CURRENT APPLICATION NUMBER: US/10/425,114  
;; CURRENT FILING DATE: 2003-04-28  
;; NUMBER OF SEQ ID NOS: 73128  
;; SEQ ID NO 58160  
;; LENGTH: 324  
;; TYPE: PRT  
;; ORGANISM: Zea mays  
;; FEATURE:  
;; OTHER INFORMATION: Clone ID: UC-ZMFLB73219F07\_FLI.pep  
US-10-425-114-58160

Alignment Scores:  
Pred. No.: 2.95e-05 Length: 324  
Score: 148.00 Matches: 62  
Percent Similarity: 38.1% Conservative: 18  
Best Local Similarity: 29.5% Mismatches: 77  
Query Match: 13.2% Indels: 53  
DB: 4 Gaps: 10

US-09-920-953-2 (1-598) x US-10-425-114-58160 (1-324)

QY 5 TGCCTGCAGACGGG-----CCACGAGCACACAGAGCGCGGAACGG 49  
DB 84 CysAlaArgThrArgAlaArgThrAlaProSerAlaProCysThrArgArgThr 103  
QY 50 GATCGGCGCAAGAAGCTGTTTGTGACCTGGCGCGCGCAGAGGATGAAGCTGGCGG 109  
DB 104 SerSerGlySerArgAlaCys-----CTGACCCGAGCTGCTGC 110  
QY 110 TTGACACCTTCTACGATAAGTCTGG-----CTGACCCGAGCTGCTGC 154  
DB 111 -----ProSerAlaAlaThrCysTyrArgTyrPalaAlaThrArgSerArgProThrSer 128  
QY 155 CCTTCTTCGAGTCCCTGACATCAAGAGCAGAGATGAAGCAGGTCAAGTTCATGAGCT 214  
DB 129 ProArgTyrGlyProTyrCysCysProSerProSer---SerCysSerSerSerArgAla 147  
QY 215 TCCTGTTTGGCGGAGCAGACCAATACAAAGGCGCGAAGCATGTACGACGACACGCCCATC 274  
DB 148 CysCysSerAlaThrCysSerArgProArg-ProProArgArgArgArgProProG 167  
QY 275 TGGT-----CAAGGCCACGGCTGGACCGCCACTTTTGACAAGATCAAGCAGTACC 328  
DB 167 nGlyThrProArgProArgPro---ThrSerArgThrSerSerAlaArgSerSerThr 186  
QY 329 TTGACGAGAGCGCTGCAAGAGA-----TGGCGCTCAAGCAGGATGTGATCC 373  
DB 187 -----SerAlaCysThrArgProAlaAlaThrCysTyrSerThrCysArgAlaThrTyr 204  
QY 374 AGCACCGCCCGGAGTGTGGAGTCCACCGCGCAGCAATTTGACTTNCACCAACACTGCG 433  
DB 205 AlaCysAlaThrProThrTyrArgProProAlaProArgCysThrAlaSerAlaThr--- 223  
QY 434 CACCAACTGATTTTCATTAACCAACCCAGCTGAGCGCTCATTCCTCATTTTGAG 493  
DB 224 -----ProGlnAlaAlaAlaSerGlyThrSerTyrArg 234  
QY 494 -----CGGGAGCGCCAGTTCGCGAGCGCGCCAGCGCGCCAGGAGCTGCA 541  
DB 235 ThrTyrArgProArgAlaAlaSerAlaAlaAlaThrAlaSerGlySer---SerProSer 253  
QY 542 AATCGTTTCCAGCCCTTGTGCA 565  
DB 254 GlyArgAlaSerSerAlaThrAla 261

## RESULT 3

US-11-096-568A-19503  
;; Sequence 19503, Application US/11096568A  
;; Publication No. US20060048240A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Alexandrov, Nikolai et al.  
;; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
;; TITLE OF INVENTION: Therby  
;; FILE REFERENCE: 2750-1592PUS2  
;; CURRENT APPLICATION NUMBER: US/11/096,568A  
;; CURRENT FILING DATE: 2005-04-01  
;; NUMBER OF SEQ ID NOS: 34471  
;; SEQ ID NO 19503  
;; LENGTH: 428  
;; TYPE: PRT  
;; ORGANISM: Zea mays subsp. mays  
;; FEATURE:  
;; NAME/KEY: misc\_feature

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; LOCATION: (1)..(428)
; OTHER INFORMATION: Ceres Seq. ID no. 12373378
US-11-096-568A-19503

Alignment Scores:
Pred. No.: 3,17e-05 Length: 428
Score: 148.00 Matches: 62
Percent Similarity: 38.1% Conservative: 18
Best Local Similarity: 29.5% Mismatches: 77
Query Match: 13.2% Indels: 53
DB: 6 Gaps: 10

US-09-920-953-2 (1-598) x US-11-096-568A-19503 (1-428)
QY 5 TGCCTGCAGACGGG-----CCACCAGCACACAGACGCGCGGAAGCGG 49
Db 221 CysAlaArgThrArgAlaArgThrAlaProSerAlaProCysThrArgArgThr 240
QY 50 GATCGGCGCAAGAGCTGTTGATGACCTGGCGCGCAGAGGCGATGAAGCTGGCGG 109
Db 241 SerSerGlySerArgAlaCys-----
QY 110 TTGACACCTTCTACGATAAGTGCTGG-----CTGACCCGGAGCTGCTGC 154
Db 248 -----ProSerAlaAlaThrCysTrpArgTrpAlaAlaThrArgSerArgProThrSer 265
QY 155 CCTTCTTCGAGTCCCTGGACATGCAAGACGAGAAGATGAAGCTCAAGTTCTAGACT 214
Db 266 ProArgTrpGlyProTrpCysCysProSerProSer---SerCysSerSerArgAla 284
QY 215 TCGTGTGTTGGCGGAGCAGCAATACAGGCGCGCAAGCATGTACGACGACACGCCCATC 274
Db 285 CysCysSerAlaThrCysSerArgProArg-ProProArgArgArgArgProProGl 304
QY 275 TGGT-----CAAGGGCCACGGCTGGACACCCGCAATTTGACTTNCACCAACTGCG 328
Db 304 nGlyThrProArgProProArgPro--ThrSerArgThrSerSerAlaArgSerThr 323
QY 329 TTGAGAGACGCTCAAGAGA-----TGGCGCTCAAGCAGGATGTGATCC 373
Db 324 -----SerAlaCysThrArgProAlaAlaThrCysTrpSerThrCysArgAlaThrTrp 341
QY 374 AGCAGCGCGCGGAGTGGTGAGTCCACCGCGAGCAATTTGACTTNCACCAACTGCG 433
Db 342 AlaCysAlaThrProThrTrpArgProProAlaProArgCysThrAlaSerAlaThr--- 360
QY 434 CACCCAACTGATTTTCATTAAACCCACCCAGCCCTGAGCGCTCATTCATCGATTTCAG 493
Db 361 -----ProGlnAlaAlaSerGlyThrSerTrpArg 371
QY 494 -----CGGGAGCGCCAGTTGCCGAGCGCGCCAGGCGCGCCAGGAGCGCTGCA 541
Db 372 ThrTrpArgProArgAlaAlaSerAlaAlaAlaThrAlaSerGlySer---SerProSer 390
QY 542 AATCGTTTGCAGCCCTTGCTGCA 565
Db 391 GlyArgAlaSerSerAlaThrAla 398

RESULT 4
US-11-096-568A-19501
; Sequence 19501, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19501
; LENGTH: 544
; TYPE: PRt
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; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(544)
; OTHER INFORMATION: Ceres Seq. ID no. 12373376
US-11-096-568A-19501

Alignment Scores:
Pred. No.: 3,37e-05 Length: 544
Score: 148.00 Matches: 62
Percent Similarity: 38.1% Conservative: 18
Best Local Similarity: 29.5% Mismatches: 77
Query Match: 13.2% Indels: 53
DB: 6 Gaps: 10

US-09-920-953-2 (1-598) x US-11-096-568A-19501 (1-544)
QY 5 TGCCTGCAGACGGG-----CCACCAGCACACAGACGCGCGGAAGCGG 49
Db 337 CysAlaArgThrArgAlaArgThrAlaProSerAlaProCysThrArgArgThr 356
QY 50 GATCGGCGCAAGAGCTGTTGATGACCTGGCGCGCAGAGGCGATGAAGCTGGCGG 109
Db 357 SerSerGlySerArgAlaCys-----
QY 110 TTGACACCTTCTACGATAAGTGCTGG-----CTGACCCGGAGCTGCTGC 154
Db 364 -----ProSerAlaAlaThrCysTrpArgTrpAlaAlaThrArgSerArgProThrSer 381
QY 155 CCTTCTTCGAGTCCCTGGACATGCAAGACGAGAAGATGAAGCTCAAGTTCTAGACT 214
Db 382 ProArgTrpGlyProTrpCysCysProSerProSer---SerCysSerSerArgAla 400
QY 215 TCGTGTGTTGGCGGAGCAGCAATACAGGCGCGCAAGCATGTACGACGACACGCCCATC 274
Db 401 CysCysSerAlaThrCysSerArgProArg-ProProArgArgArgArgProProGl 420
QY 275 TGGT-----CAAGGGCCACGGCTGGACACCCGCAATTTGACTTNCACCAACTGCG 328
Db 420 nGlyThrProArgProProArgPro--ThrSerArgThrSerSerAlaArgSerThr 439
QY 329 TTGAGAGACGCTCAAGAGA-----TGGCGCTCAAGCAGGATGTGATCC 373
Db 440 -----SerAlaCysThrArgProAlaAlaThrCysTrpSerThrCysArgAlaThrTrp 457
QY 374 AGCAGCGCGCGGAGTGGTGAGTCCACCGCGAGCAATTTGACTTNCACCAACTGCG 433
Db 458 AlaCysAlaThrProThrTrpArgProProAlaProArgCysThrAlaSerAlaThr--- 476
QY 434 CACCCAACTGATTTTCATTAAACCCACCCAGCGCTGAGCGCTCATTCATCGATTTCAG 493
Db 477 -----ProGlnAlaAlaSerGlyThrSerTrpArg 487
QY 494 -----CGGGAGCGCCAGTTGCCGAGCGCGCCAGGCGCGCCAGGAGCGCTGCA 541
Db 488 ThrTrpArgProArgAlaAlaSerAlaAlaAlaThrAlaSerGlySer---SerProSer 506
QY 542 AATCGTTTGCAGCCCTTGCTGCA 565
Db 507 GlyArgAlaSerSerAlaThrAla 514

RESULT 5
US-10-084-846A-5
; Sequence 5, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MOHLENWEG, AGNES
; APPLICANT: TREFFZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
```



```
Oy 31 TGGTCTGTGG 20
Db 186 TrpSerTrpTrp 189

RESULT 7
US-11-096-568A-8162
; Sequence 8162, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096, 568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 8162
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(210)
; OTHER INFORMATION: Ceres Seq. ID no. 15177853
US-11-096-568A-8162

Alignment Scores:
Pred. No.: 0.00232 Length: 210
Score: 128.00 Matches: 55
Percent Similarity: 36.9% Conservative: 20
Best Local Similarity: 27.1% Mismatches: 75
Query Match: 11.4% Indels: 53
DB: 6 Gaps: 9

US-09-920-953-2 (1-598) x US-11-096-568A-8162 (1-210)

Oy 530 GGGCCCCCTGGCGCTCGCACTGGCGCTCCCGCTCAAAATCGATGATGAGCGC 471
Db 13 GlyArgGlyGlnAlaArgSerGluInProTrpLeuArgArgTrpProArg 32
Oy 470 -----TCAGGCTGGGGTTGG---GTTAATGAAATCACTGGTGGCGCAGTTG 426
Db 33 ArgAlaArgSerSerGlyProGlyTrpArgThrArgArgArgThrGlyAlaSerTrp 52
Oy 425 TTGGGNAAG----- 417
Db 53 ArgGlySerAlaSerAlaArgArgProArgArgArgProArgProArgPro 72
Oy 416 -----TCAATTCGTGGCGGTGGACTCCACACTCCGGCGCGTGC 375
Db 73 ProThrGlyArgCysGlySerProAlaArgArgProSerThrSerThrGlyArgSer 92
Oy 374 TGGATCATCTGCTTCAGCGCCATCTTTCAGCGGCTCTCCAAAGTACTGCTTGATC 315
Db 93 SerAlaThrAlaSerThrPro---SerAlaLeuGlySerProArgSerThrCysSer 111
Oy 314 TTGTCAAAGTGGCGGTGGTCCAGGCGGTGGCCCTTGACACAGATGGCGTGTGCGTGTAC 255
Db 112 ThrThrTrpTrpProTrpThrArgThrTrpProArgThr---TrpArgAlaArgSer--- 129
Oy 254 ATGCTTGGCCCTGTATGTGTCTGCTCCG-----CCAAACAGAAAGTCTATG 207
Db 130 -----SerAlaProGlySerArgThrProThrSerSerProPro 142
Oy 206 AACTTGACCTGCTTCATCTTCTGCTGTGATGTCAGGACTCGAAGAGGCGAGCAGC 147
Db 143 ArgSerSerProThrProArgCysSer-----AlaSerArgGlySerAla 157
Oy 146 TCCGGGTGAGGAGCAGCCTTATCTAGAGAGTGTCAACCGCAGCTTCACTGCTTCTGCG 87
Db 158 SerAlaSerSerThrValAla-GlyProCysSerProProSerAla----- 173
Oy 86 CCGCCAGGTATCAAAACAGCTTCTTGGCGCGGATCCCGCTTCCGCGCTCTCTGTGGTG 27
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Db 174 ----ProSerProSerSerGlySerProAlaSerProGlyArgThrProAlaArgTrpSe 192
Oy 26 CTGGTG 20
Db 192 rTrpTrp 194

RESULT 8
US-10-437-963-143835
; Sequence 143835, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 143835
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_44705C.1.pep
US-10-437-963-143835

Alignment Scores:
Pred. No.: 0.00543 Length: 417
Score: 125.00 Matches: 63
Percent Similarity: 36.2% Conservative: 13
Best Local Similarity: 30.0% Mismatches: 74
Query Match: 11.1% Indels: 60
DB: 4 Gaps: 10

US-09-920-953-2 (1-598) x US-10-437-963-143835 (1-417)

Oy 23 CCAGCACACAGACGCGGAGCGGGATGCGGGCGCAAGAAAGCTGTTGATGACCTGG 82
Db 22 ProThrProHisArgArgGlu-----IleGluArgTrp 32
Oy 83 GCGCGCGAGAGGATGAGCTGGCGTTGACACTTCTAGCATAGGTGCTGGTGACC 142
Db 33 Leu-----ProTrpArgSerAlaProPro-----ThrThr 43
Oy 143 CGGAGCTGCTGC-----CCTTCTTCGAGTCCCTCGACATGCAAGAGCAGA 187
Db 44 GlySerCysSerThrProThrThrProProProProProProProProProProPro 62
Oy 188 AGATGAAGCAGGTTCAGTTCATGAGCTTCGTGTTTGGCGGAGCAGACCAATACAGGGCC 247
Db 63 -----SerArgSerLeuProAlaThrProProProAlaProThrLysArgArg--- 79
Oy 248 GAAGCATGTACGACGACACGCCCATCTGTTCAAGGCGCAGCGGCTGGACCCGCGCACT 307
Db 80 -----ArgThrThrArgTrp---GlyAlaThr 87
Oy 308 TTGCAAGATCAACAGCTACTCTGGAG-----AGACGCTGCAAG 346
Db 88 LeuThrAlaThrThrSerThrAlaGluAsnSerArgArgArgThrArgArgAlaArgArg 107
Oy 347 AGATGGCGGTCAAGCAGGATGTGATCCAGCAGCGCGCGGAGTGGTGGAGTCCA----- 400
Db 108 ArgArgGlyArgSerArgAlaSerSerThrThrProProProProProProProProPro 127
Oy 401 ---CCCGCGAGAAATTTGACTTTCCTTCCCAACAACTGCGCACCACTGATTTTCAATAACC 457
```

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Db 128 SerProSerThrProSerAlaAlaProSerThrSerSerProThrArgAlaSerProPro 147
|||:||||| |||:||||| |||:||||| |||:|||||
458 AACCCCGCTGAGCGCTCATTCATCGATTTGAGCGGGGAGCGCCAGTTCGCCGAGCGC 517
|||:||||| |||:||||| |||:||||| |||:|||||
148 TyrArgSerThrSerProSerSerProPro--ProAlaAlaSerSerAlaAlaAla 167
|||:||||| |||:||||| |||:||||| |||:|||||
518 GCCAGGGGGGCCA-----GGAGCCTGCAAAATCGTTTG 550
|||:||||| |||:||||| |||:||||| |||:|||||
167 rGProProAlaProThrThrSerProThrArgProProSerSerGlyGlyCysAlaSerLeuA 187
|||:||||| |||:||||| |||:||||| |||:|||||
551 CCAGCCCTTGCTGCATTGAAGAGCCA 576
|||:||||| |||:||||| |||:||||| |||:|||||
187 laThrProAlaThrThrSerThrPro 195

RESULT 9
US-10-084-846A-3
; Sequence 3, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084, 846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 19695
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
US-10-084-846A-3

Alignment Scores:
Pred. No.: 0.0147 Length: 19695
Score: 125.00 Matches: 57
Percent Similarity: 35.3% Conservative: 15
Best Local Similarity: 27.9% Mismatches: 68
Query Match: 11.1% Indels: 64
DB: 4 Gaps: 11

US-09-920-953-2 (1-598) x US-10-084-846A-3 (1-19695)
QY 2 CGTGTCTGCAGAGC---CGGCCACAGACACAGCGGGAAGCGGATGCGGGC 58
||||| |||:||||| |||:||||| |||:|||||
Db 11324 ArgCysAlaGlyThrSerAlaSerProAlaSerThrArgSerArgSerProAla 11343
||||| |||:||||| |||:||||| |||:|||||
QY 59 GCAAGA-----AGCTGTTGTGATCACCTGGCGCGGCGCAGAGGCGTAAGC 103
||||| |||:||||| |||:||||| |||:|||||
Db 11344 AlaArgThrTrpArgCysGlyAlaAlaSerThrThrTrpAlaAlaGlyArg----- 11361
||||| |||:||||| |||:||||| |||:|||||
QY 104 TGGCGGTGACACCTTCTACATAAGG-----TGCTGG----- 136
||||| |||:||||| |||:||||| |||:|||||
Db 11362 -----SerAlaValArgLysAsnCysTrpSerSerSerThrProArgPro 11376
||||| |||:||||| |||:||||| |||:|||||
QY 137 -----CTGACCGGAGCTGCTGCTTCTTCTCGAGTCCCTCGACATGC 178
||||| |||:||||| |||:||||| |||:|||||
Db 11377 ProThrSerGlySerSerThrThrArgAlaValCysGlyAlaGlySerThrTrpPro 11396
||||| |||:||||| |||:||||| |||:|||||
QY 179 AAGAGCAGAAGTGAAGCAGTCAAGTTCA-----TGAGCTTCGTGTTG 223
||||| |||:||||| |||:||||| |||:|||||
Db 11397 AspSerSerProCysProArgCysSerSerTrpThrProProAlaSerThrArg 11416
||||| |||:||||| |||:||||| |||:|||||

QY 224 GCGAGCAGAGC-----AATCAAGGGCGCGAAGCATGT 256
||||| |||:||||| |||:||||| |||:|||||
Db 11417 AlaThrAlaThrArgSerGlyArgTrpSerValArgTrpSerArgAlaProProCys 11436
||||| |||:||||| |||:||||| |||:|||||
QY 257 ACAGCGCACACGCCCATCTCGTCAAGGCCACCGCTGGACCCGCTTTGACAAGA 316
||||| |||:||||| |||:||||| |||:|||||
Db 11437 CysSerProArgSerThrTrpArgA-g-----ProThrGlySerProThrArg 11452
||||| |||:||||| |||:||||| |||:|||||
QY 317 TCAAGCAGTACTTGGAGAGACGCTCAAGAGATGGCGTCAAGCAGGATGTGATCCAGC 376
||||| |||:||||| |||:||||| |||:|||||
Db 11453 SerArgSerThr-----ArgAlaAlaGlySerSerArgAlaProPro 11466
||||| |||:||||| |||:||||| |||:|||||
QY 377 ACGCCCGCGAGTGTGGAGT-----CCACCGCGCAGC--- 409
||||| |||:||||| |||:||||| |||:|||||
Db 11467 ArgProSerProTrpTrpAlaAlaThrGlySerTrpTrpArgProProArgThrCys 11486
||||| |||:||||| |||:||||| |||:|||||
QY 410 -----AATTTGACTTNCACCAACTGCGCACCAACTGATTTTCATTAAACCCAAC 460
||||| |||:||||| |||:||||| |||:|||||
Db 11487 ArgProProArgLeuArgSerProAlaSerArgGlyProSerProArgTrpThrProArg 11506
||||| |||:||||| |||:||||| |||:|||||
QY 461 CCAGCCTGAGC 472
||||| |||:||||| |||:||||| |||:|||||
Db 11507 ProAlaValSer 11510
||||| |||:||||| |||:||||| |||:|||||

RESULT 10
US-10-084-846A-6
; Sequence 6, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084, 846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 19662
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 2.
; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
US-10-084-846A-6

Alignment Scores:
Pred. No.: 0.0165 Length: 19662
Score: 124.50 Matches: 56
Percent Similarity: 33.0% Conservative: 14
Best Local Similarity: 26.4% Mismatches: 64
Query Match: 11.1% Indels: 78
DB: 4 Gaps: 10

US-09-920-953-2 (1-598) x US-10-084-846A-6 (1-19662)
QY 536 GTCCTGGCGCCCTGGGCGCGCTCGCAACTGGCG---CTCCCCGCTCAAAATCGATGG 480
||||| |||:||||| |||:||||| |||:|||||
Db 19332 AlaProGlyArgProProArgProArgProCysAlaGlyPheProThr----- 19347
||||| |||:||||| |||:||||| |||:|||||
QY 479 AATGACGCTCAGGCTGGGTTGGGTTAATGAAATCAGTTGGGTGGCGAGTTGTTGGN 420
||||| |||:||||| |||:||||| |||:|||||
Db 19348 -----ProGlyProGlyTrp----- 19352
||||| |||:||||| |||:||||| |||:|||||
QY 419 AAGTCAATTCGTGGCGGTGGACTCCACCACTCCGCGCGCGTGTGGATCATCATCC--- 363
||||| |||:||||| |||:||||| |||:|||||
Db 19353 -----AlaAlaAlaCysSerAlaAlaProCysSerCysSerAlaThrSerThr 19368
||||| |||:||||| |||:||||| |||:|||||
```

QY 362 -----TGCTTGAGCGCCATCTCTTCGAGGGTCTCTCCA 330  
Db 19369 ArgCysSerGlyArgSerArgCysThrAlaCysCysSerProCysAlaSer 19388  
QY 329 AGGTACTGC---TTGATCTTGTCAAAGTGGCGG-----TGGTCCAGG----- 291  
Db 19389 ArgArgCysGlyCysAlaGlyAlaThrTrpArgProArgTrpTrpTyArgSerPro 19408  
QY 290 ---CCGTGGCCCTTGACAGATGGCGGTGCGTCGTACATGCTTCGGCCCTTGATGG 234  
Db 19409 SerProTrpGlyTrpCysArgTrpProThrAlaAlaGlyGlySerAlaAspThrTrpGly 19428  
QY 233 TCTGCTCGCCCAACACG----- 216  
Db 19429 SerSerProSerProArgProGlyGlyCysThrGluGlyArgSerProValSer 19448  
QY 215 -----AAGCTCATGAACCTTGACCTGCCTTCATCTCTCTCTCTGTCATGCTCCAGG 168  
Db 19449 SerProHisGlyArg-SerGlyCysTrpProAlaGlyProArgProAlaAlaGlyProGly 19468  
QY 167 GACTCGAAGAGGCACAGCTCGGTCAGCCAGCCACCTTATCGTAGAAGGTGTCAACC 108  
Db 19468 YAspArgArgGlnAlaLeuSerSerGlySerPro----- 19479  
QY 107 GCAGCTTCATGCTCTGCGCCGCCAGGTGCATCAACAGCTTCTTGGCGCCGCTCC 48  
Db 19480 -----ArgArgArgGlyAlaProSerPheSerAlaAlaArgGlyAl 19493  
QY 47 GCTTCCG-----CCGTCTCTGCTGCTGCTGGTGG 20  
Db 19493 aAlaProThrIleProAlaLeuPheCysSerTrp 19504

## RESULT 11

US-10-084-846A-8  
; Sequence 8, Application US/10084846A  
; Publication No. US20040006026A1  
; GENERAL INFORMATION:  
; APPLICANT: WEITNAUER, GABRIELE  
; APPLICANT: MUHLENWEG, AGNES  
; APPLICANT: TREFFER, AXEL  
; APPLICANT: BECHTHOLD, ANDREAS  
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES  
; FILE REFERENCE: 1974-005  
; CURRENT APPLICATION NUMBER: US/10/084, 846A  
; PRIOR FILING DATE: 2003-02-25  
; PRIOR APPLICATION NUMBER: PCT/EP01/09815  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: DE 101 09 166.4  
; PRIOR FILING DATE: 2001-02-25  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 8  
; LENGTH: 19608  
; TYPE: PRT  
; ORGANISM: Streptomyces viridochromogenes  
; FEATURE:  
; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.  
; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.  
US-10-084-846A-8

Alignment Scores:  
Pred. No.: 0.0403 Length: 19608  
Score: 120.50 Matches: 49  
Percent Similarity: 35.7% Conservative: 16  
Best Local Similarity: 26.9% Mismatches: 92  
Query Match: 10.7% Indels: 25  
DB: 4 Gaps: 7

US-09-920-953-2 (1-598) x US-10-084-846A-8 (1-19608)

QY 20 CCACGACACACAGACGCGGAGCGGATGCGGCGGACAGACGCTGTTGTATGACC 79  
::: |||

Db 5430 ProProAla-----SerSerThrArgCysCys----- 5438  
QY 80 TGGCGCGCAGAGCATGAAGCTGCGGTGACACCTTCTACGATAGGTGCTGGCTG.139  
Db 5439 -----ProProAlaSerThrTrpArg-----SerThrAlaAlaCysTrpPro 5452  
QY 140 ACCCGAGCTGCTGCGCTTCTCGAGTCCCTGACATGCAAGAGCAGAGATCAAGCAGG 199  
Db 5453 ArgArgProCysSerProArgThrArg-----ThrSerArgArgArgArgProGlyArg 5470  
QY 200 TCAAGTTTACGACTTCGTGTTTG---GCGGAGCAGACCAATACAAAGGCCGCGCATGT 256  
Db 5471 SerThrSerArgSerThrAlaThrProThrSerGlyCysSerProTrpCysProAlaCys 5490  
QY 257 ACAGCCACACGCCCATCTGTCAGGCGCACGGCTTGACACCGCCACTTTTGACAAGA 316  
Db 5491 ThrSerAspArgProAlaArgProProThrSerSerTrpProThrArgProArgSerAla 5510  
QY 317 TCAAGCAGTACCTTGAGAGAGCGCTCAAGAGATGGCGTCAAGCAGGAGTGTATCCAGC 376  
Db 5511 ProArgProSerThrSerArgSerThrAlaArgTrpProSerProAsnTrpSerArgAsp 5530  
QY 377 AGCGCCCGGAGTGGTGGAGTCCACCCGCGACGAATTTGACTTNNCCCAACA-----ACT 430  
Db 5531 TrpProThrSerThrThrProSerProAlaAlaArgThrArgThrAlaProSerArgArgThr 5550  
QY 431 GCGCACCCAACTGATTTTTCATTAACCCACCCAGCTGAGCGCTCATTCATCGATTTT 490  
Db 5551 ProArgProThrProCysArgArgThrThrProSerAlaSerCysSerArg----- 5567  
QY 491 GAGCGGGAGCGCGCAGTTCGCGAGCGCGCCAGCGGGGCCAGGAGCTGCAAAATCGTTTG 550  
Db 5568 ArgProArgThrProValTrpArgArgProGlyCysProHisArgSerAlaArgLeu 5587  
QY 551 CCAGCC 556  
Db 5588 ProAla 5589

## RESULT 12

US-11-096-568A-23618  
; Sequence 23618, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; TITLE OF INVENTION: Therby  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 23618  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(375)  
; OTHER INFORMATION: Ceres Seq. ID no. 12414168  
US-11-096-568A-23618

Alignment Scores:  
Pred. No.: 0.0162 Length: 375  
Score: 120.00 Matches: 56  
Percent Similarity: 37.2% Conservative: 21  
Best Local Similarity: 27.1% Mismatches: 92  
Query Match: 10.7% Indels: 38  
DB: 6 Gaps: 8

US-09-920-953-2 (1-598) x US-11-096-568A-23618 (1-375)

QY 5 TGCTGACGCGCGGCCACCCAGCAGCAGCGGCGGAGCGGATGCGGGCGCAAGA 64  
Db 172 CysArgAlaThrArgProAlaAlaProSerArgThrThrSerProCysAla----- 188



QY 65 AGCTGTTGATGACCTGGCGGCGCAGAGGATGAAGCTGGCGGTTGACACCTTCTACG 124  
Db 189 -----SerValAlaArgProArgThrTrpProProSerPro----- 200  
QY 125 ATAAGGTGCTGGCTGACCGGAGCTGCTCTTCGAGTCCCTCGACATGCAAGAGC 184  
Db 201 -----CysGlyAspThrSerSerSerCysHisSerSerAlaAlaTrpArgAlaArgGly 218  
QY 185 AGAAGATGAAGCAGGTCAAGTTCATGAGTTCGTTGTTGGCGGAGCAGACCAATACAAG 244  
Db 219 ArgArgProSerAlaProProThrLeuSerSerThrGlyProSerThrAlaAlaThrGly 238  
QY 245 GCCGAGCATGTACGACGCGACACGCCCATCTGTCAGGCGCCAGGCTCGACACCGCC 304  
Db 239 AlaCysArgCys-----ArgArgAlaProArgProThrThrPro 251  
QY 305 ACTTTCACAAGATCAAGCAGTACCTTGGAGAGAGCTGCAAGAGATGGCGGTCAAGCAGG 364  
Db 252 TrpProThrArgSerAlaProAlaArg-----ArgArgTrpThrProSer--- 266  
QY 365 ATGTGATCCAGCAGCGCGCGAGTGTGTGAGTCCACCCCG-----ACGAATTTG 415  
Db 267 -----SerSerArgProPro-----TrpSerSerAlaAlaAlaThrSerSerThr 282  
QY 416 ACTTNGCCAACTGGCGCACCACTGATTTTCATTAACCCACCCAGCCTGAGCGCT 475  
Db 283 ThrAlaProSerThrThrProProGlySerGlyProProGlySerProSerTrpSerGly 302  
QY 476 CATTCATCATGATTTGAGCGGGAGCG-----CCAGTTGCGGAGCGC 517  
Db 303 ThrSerThrAlaSerSerThrAlaSerSerProSerSerThrProGlyProThrProPro 322  
QY 518 GCCAGGGGCGCCAGGAGCTGCAATCGTTTGCAGCCCTTCTGCAATTGAAGAGCCAT 577  
Db 323 SerSerCysAlaSerSerSerAlaSerSerThrProThrAlaAlaSerThrSerThrAsp 342  
QY 578 CAGCCATTTTCGACCAAGCC 598  
Db 343 ThrSerValSerAsnSerSer 349

RESULT 13  
US-10-437-963-166380  
; Sequence 166380, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 166380  
; LENGTH: 276  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(276)  
; OTHER INFORMATION: unsure at all xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_65095C.1.pap  
US-10-437-963-166380

Alignment Scores:

Pred. No.: 0.0167 Length: 276  
Score: 119.50 Matches: 52  
Percent Similarity: 35.1% Conservative: 15  
Best Local Similarity: 27.2% Mismatches: 69  
Query Match: 10.7% Indels: 55  
DB: 4 Gaps: 8  
US-09-920-953-2 (1-598) x US-10-437-963-166380 (1-276)  
QY 29 CCACAGAGCGCGGAGCGGATGCGGCGCAAGAAGCTGTTTGATGACCTGGCGGCGG 88  
Db 3 ProArgArgArgArgArgArgileCysThrValArg----- 14  
QY 89 CAGAAGGCATGAAGCTGGCGGTTGACACCTTCTACATAAGGTGCTGGTGAACCCGAGC 148  
Db 15 -----ArgProThrAlaThrThr-----ThrThrThrSer 25  
QY 149 TGCTGCTCTTTCGAGTCCCTGGACATGCAAGACGAGAGATGAAGCAGGTCAAGTTCA 208  
Db 26 AlaSerProSerSerSerProThrPro-----GlySerSerProGly 39  
QY 209 TGAGCTTCGTGTTGCGGAGCAGACCAATACAAGGCGCGAGCATGTACGACG----- 262  
Db 40 AlaAlaSerCysAlaThrSerSerAlaAlaSerAlaThrArgThrSerThrAlaPro 59  
QY 263 ---CACAGCCCATCTGTCAAGGCGCCAGCGCTCGACCCACCGCCTTTGACAAATCA 319  
Db 60 ProSerSerProSerHisGlySerArgSerProTrpThrGlyThrThrSerSerProSer 79  
QY 320 AGCAGTACCTTGGAGAGCGCTGC-----AAGAGATGGCGCTCAAGCAGGAGTGCA 370  
Db 80 ArgSerGlySerCysArgGlyCysCysPheArgArgTrpArgSerThrArg----- 97  
QY 371 TCCAGCAGCGCGCGGAGTGTGGAGTCCACCGCGCAGCAATTTGACTTNCACCAACT 430  
Db 98 -----ProAlaAlaProSerSerAlaSerProThrGly 108  
QY 431 GGCACCCCACTGATTTTCATTAAACCCACCGCCTGAGCGCTCATTCATCGATTTT 490  
Db 109 AlaSerThrThrSer-----ProSerProThr----- 117  
QY 491 GAGCGGAGCGCCAGTGTGCGAGCGCGCCAGGCGCCAGGAGCTCTCAATCGTTTG 550  
Db 118 -----ProAlaAlaArgAlaAlaSerGlyAlaProAlaAspGlySer\*\*\*Cys 133  
QY 551 CCAGCCCTTGTGCTGATTGAAGAGCCATCAGCCA 583  
Db 134 SerGlyArgAlaProArgGluSerSerAlaPro 144  
RESULT 14  
US-11-096-568A-18960  
; Sequence 18960, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nickolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; TITLE OF INVENTION: Therby  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 18960  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(309)  
; OTHER INFORMATION: Ceres Seq. ID no. 12367975  
US-11-096-568A-18960  
Alignment Scores: 0.027 Length: 309  
Pred. No.:

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Score: 117.50 Matches: 75
Percent Similarity: 36.7% Conservative: 15
Best Local Similarity: 30.6% Mismatches: 86
Query Match: 10.5% Indels: 69
DB: 6 Gaps: 13

US-09-920-953-2 (1-598) x US-11-096-568A-18960 (1-309)

QY 15 CGCGGCCACACGAC-----CACAGAGCGCGGAGCGGATGCGGCGCAAGAAGCT 68
Db 57 ArgGlyHisArgHisProSerHisArgProLeuAlaSerValArgGln-----72
QY 69 GTTTGATGACCTGGCGGCGCAGAGGCGATGAAGCTGGC-----107
Db 73 -----ArgArgArgArgGlyArgAlaGlyArgArgGlyGlyArgGlyGlu 87
QY 108 ---GGTTGACACCTTCTACGA-----TAAGGTGCT 134
Db 88 ProGlyLeuGlyLeuLeuArgGlyArgGlyProArgArgAlaArgAspHisGlyAla 107
QY 135 GCGTGACCGGAGCTGCTGCTTTCGAGTCCCTGGACATGCA-----AGAGCA 185
Db 108 ArgAspGlyGlyAlaAlaArgValLeuArgAlaAlaGlyArgAlaGlyArgAla 127
QY 186 GAAGATCAACGAGCTCAAGTTTCATGAGCTTCGTTTGGCGGACACCA-----236
Db 128 GluGluArgGlyGlyAlaAlaArgValLeuArgValGlyAlaHisGlnGluArgGly 147
QY 237 ATCAAGGGCGGAGCATGTACGACGACACGCGCCATCTGCTCAAGGGCGCCGCTGGA 296
Db 148 LeuGluGlyGlyValArgProArgAlaAlaArgAlaAlaAlaGlyCysArgGlyArg 167
QY 297 CCACCGCCACTTTGACAAGATCAAGCAGTACCT-----TGAGAGAGCGCT 341
Db 168 ArgArgAlaArgValArgGluGlnValAlaProGlySerAlaGlyLeuGlnArgGlyAla 187
QY 342 GCA-----AGAGATGGCGT-----CAACGAGATGTGATCCAGCA 377
Db 188 GlyGlyValArgGlnSerAspGlyArgAlaGlyValGlnAlaAlaAlaAlaAlaAla 207
QY 378 CGCGCGCGGAGTGGTGGAGTCCACCGCGACGAAT---TTGACTTNCACCAACCTGCGC 434
Db 207 erGluProGluAlaGluAlaArgProAlaAlaArgLeuLeuGlnGlyProAspLeuH 227
QY 435 ACCCACTGTTTTCATTAAACCAACCCAGCTGAGCGCTCATTCATCGATTTTGAGC 494
Db 227 isProAlaGlu-----ProLeuProSerLeuProGluProArgProGlyProArg 244
QY 495 GCGGAGCG-----CCAGTTGCGGAGCGCGCCGAGGGG 527
Db 244 rgGlyAlaAlaGlnGlyArgArgProAspHisProValProGlyArgArgGlyAla 264
QY 528 CCAGGAGCGCTGCA-----AATCGTTTCCAGCGCTTTCGTCATTGA 569
Db 264 laArgArgProAlaAlaLeuArgArgValGlyProArgGlnAlaArgAlaArgLeuV 284
QY 570 AGAGCCATCAG 580
Db 284 alHisHisGln 287

RESULT 15
US-10-425-114-72136
; Sequence 72136, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

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; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72136
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3245-558-Al_FLI.pep
US-10-425-114-72136

Alignment Scores:
Pred. No.: 0.0285 Length: 384
Score: 117.50 Matches: 69
Percent Similarity: 37.9% Conservative: 16
Best Local Similarity: 30.8% Mismatches: 74
Query Match: 10.5% Indels: 65
DB: 4 Gaps: 13

US-09-920-953-2 (1-598) x US-10-425-114-72136 (1-384)

QY 15 CGCGGCCACACGAC-----CACAGAGCGCGGAGCGGATGCGGCGCAAGAAGCT 68
Db 54 ArgGlyHisArgHisSerHisArgProLeuAlaSerGlyArgGln-----69
QY 69 GTTTGATGACCTGGCGGCGCAGAGGCGATGAAGCTGGC-----107
Db 70 -----ArgArgArgArgGlyArgAlaGlyArgArgGlyGlyArgGlyGlu 84
QY 108 ---GGTTGACACCTTCTACGA-----TAAGGTGCT 134
Db 85 ProGlyLeuGlyLeuLeuArgGlyArgGlyProArgArgAlaArgAspArgGlyAla 104
QY 135 GCGTGACCGGAGCTGCTGCTTTCGAGTCCCTGGACATGCA-----AGAGCA 185
Db 105 ArgAspGlyGlyAlaAlaArgValLeuArgAlaAlaGlyArgAlaGlyArgAla 124
QY 186 GAAGATCAACGAGTCAAGTTTCATGAGCTTCGTTTGGCGGAGCAGACCAATACAGGG 245
Db 125 GluGluArgGlyGlyAlaAlaArgValLeuArgValGlyAlaHisGlnGluArgGly 144
QY 246 -----CCGAGCATGTACGACGCGACACGCGCCATCTGCTCAAGGGCCA 287
Db 145 LeuGluGlyGlyValArgProArgAlaAlaArgAlaAlaAlaGlySerArgGlyArg 164
QY 288 CGG-----CCTGGACACCGCCACTTTTCACAGATCAA 320
Db 165 ArgArgAlaArgValArgGluGlnValAlaProGlySerAlaGlyLeu---GlnArgGly 183
QY 321 GCAGTACCTTGGAGAGACCTCGCAGAGATGGCGT-----CAAGCAGGATGT 368
Db 184 AlaGlyGlyValArgGluSer-----AspGlyArgAlaGlyValGlnAlaGlyAla 201
QY 369 GATCCAGCAGCGCGCGGAGTGGTGGAGTCCACCGCGACGAAT---TTGACTTNCCAA 425
Db 202 Asp--ArgProGluProGluAlaGluAlaArgProAlaAlaArgLeuLeuGlnGlyPro 221
QY 426 CAACTGCGCACCACTGTTTTCATTAAACCAACCCAGCTGAGCGCTCATTCCTCATCG 485
Db 221 spAspLeuHisProAlaGlu-----ProLeuProSerMetProGlu-----234
QY 486 ATTTTGAGCGGAGCGCGCAGCTTTCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 545
Db 235 -----ProArgProGlyProArgArgGlyThrAlaGlnGlyArgArgArgProAspHisP 253
QY 546 GTTTGCCA 553
Db 253 roValPro 255

Search completed: August 11, 2006, 10:35:52
Job time : 147 secs

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GenCore version 5.1.9  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.  
 OM nucleic - protein search, using frame\_plus\_n2p model  
 Run on: August 11, 2006, 10:31:55 ; Search time 3.6 Seconds  
 (without alignments)  
 3354.382 Million cell updates/sec

Title: US-09-920-953-2  
 Perfect score: 1122  
 Sequence: 1 gcgtgctgcagcgggc.....agccattttccaccacgacc 598

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
 Ygapop 10.0 , Ygapext 0.5  
 Fgapop 6.0 , Fgapext 7.0  
 Delop 6.0 , Delext 7.0

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 479828

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
 -MODEL=frame+ n2p.model -DEV=xlp  
 -Q=/abs/ABSSWEB.spool/US0920953/runat 10082006 163820 5518/app query.fasta\_1  
 -DB=Published Applications AA New -QFMT=fastan -SURFIX=rapbn -MINMATCH=0.1  
 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
 -TRANS=human40.cdi -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100  
 -MAXLEN=2000000000 -HOST=abs02runat 10082006 163820 5518 -NCPU=6 -ICPU=3  
 -USBR=US0920953.0CGN 1.1 46 @runat 10082006 163820 5518 -LONGLOG -DEV TIMEOUT=120  
 -NO MAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
 -WAEN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7  
 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA New:

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US09\_NEW\_PUB.pcp:\*\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US06\_NEW\_PUB.pcp:\*\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US07\_NEW\_PUB.pcp:\*\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US08\_NEW\_PUB.pcp:\*\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/PCT\_NEW\_PUB.pcp:\*\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US10\_NEW\_PUB.pcp:\*\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US11\_NEW\_PUB.pcp:\*\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US60\_NEW\_PUB.pcp:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	148	13.2	428	7	US-11-056-355B-2964
2	148	13.2	544	7	US-11-056-355B-2962
3	138.5	12.3	212	7	US-11-056-355B-7635
4	136	12.1	214	6	US-10-953-349-30500
5	128	11.4	210	7	US-11-056-355B-51768
6	123.5	11.0	358	6	US-10-953-349-28428
7	120	10.7	375	7	US-11-056-355B-3621
8	117.5	10.5	309	7	US-11-056-355B-3480
9	117	10.4	325	7	US-11-056-355B-18635
1	148	13.2	428	7	US-11-056-355B-2964
2	148	13.2	544	7	US-11-056-355B-2962
3	138.5	12.3	212	7	US-11-056-355B-7635
4	136	12.1	214	6	US-10-953-349-30500
5	128	11.4	210	7	US-11-056-355B-51768
6	123.5	11.0	358	6	US-10-953-349-28428
7	120	10.7	375	7	US-11-056-355B-3621
8	117.5	10.5	309	7	US-11-056-355B-3480
9	117	10.4	325	7	US-11-056-355B-18635

c 10	117	10.4	369	7	US-11-056-355B-18634	Sequence 18634, A
c 11	117	10.4	373	7	US-11-056-355B-18633	Sequence 18633, A
c 12	115	10.2	317	6	US-10-449-902-40564	Sequence 40564, A
c 13	112.5	10.0	352	7	US-11-056-355B-16356	Sequence 16356, A
c 14	112.5	10.0	355	7	US-11-056-355B-16355	Sequence 16355, A
c 15	112	10.0	199	6	US-10-953-349-33290	Sequence 33290, A
c 16	112	10.0	199	6	US-11-056-355B-3578	Sequence 3578, Ap
c 17	111	9.9	188	6	US-10-953-349-25350	Sequence 25350, A
c 18	111	9.9	252	7	US-11-056-355B-8234	Sequence 8234, Ap
c 19	111	9.9	424	7	US-11-056-355B-16007	Sequence 16007, A
c 20	110.5	9.8	310	6	US-10-449-902-45786	Sequence 45786, A
c 21	110.5	9.8	464	6	US-10-953-349-32673	Sequence 32673, A
c 22	110.5	9.8	464	7	US-11-056-355B-68075	Sequence 68075, A
c 23	109.5	9.8	424	7	US-11-056-355B-18007	Sequence 18007, A
c 24	108.5	9.7	291	7	US-11-056-355B-3800	Sequence 3800, Ap
c 25	108.5	9.7	345	6	US-10-953-349-30498	Sequence 30498, A
c 26	108	9.6	332	7	US-11-056-355B-51766	Sequence 51766, A
c 27	108	9.6	459	7	US-11-056-355B-5415	Sequence 5415, Ap
c 28	107.5	9.6	732	6	US-10-449-902-46957	Sequence 46957, A
c 29	107	9.5	193	7	US-11-056-355B-18087	Sequence 18087, A
c 30	107	9.5	306	6	US-10-953-349-25756	Sequence 25756, A
c 31	107	9.5	308	7	US-11-056-355B-16395	Sequence 16395, A
c 32	107	9.5	319	7	US-11-056-355B-5230	Sequence 5230, Ap
c 33	106.5	9.5	227	7	US-11-056-355B-9888	Sequence 9888, Ap
c 34	106.5	9.5	352	7	US-11-056-355B-16356	Sequence 16356, A
c 35	106.5	9.5	355	7	US-11-056-355B-16355	Sequence 16355, A
c 36	106	9.4	214	6	US-10-449-902-39304	Sequence 39304, A
c 37	106	9.4	293	7	US-11-056-355B-3637	Sequence 3637, Ap
c 38	106	9.4	457	6	US-10-449-902-41551	Sequence 41551, A
c 39	106	9.4	461	7	US-11-056-355B-6754	Sequence 6754, Ap
c 40	105.5	9.4	386	7	US-11-056-355B-16279	Sequence 16279, A
c 41	105.5	9.4	493	7	US-11-056-355B-65494	Sequence 65494, A
c 42	105	9.4	168	6	US-10-449-902-48083	Sequence 48083, A
c 43	105	9.4	288	6	US-10-953-349-26990	Sequence 26990, A
c 44	105	9.4	429	6	US-10-953-349-32400	Sequence 32400, A
c 45	104.5	9.3	353	6	US-10-449-902-53792	Sequence 53792, A

#### ALIGNMENTS

RESULT 1  
 US-11-056-355B-2964  
 ; Sequence 2964, Application US/11056355B  
 ; Publication No. US20060150283A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brover, Vyacheslav  
 ; APPLICANT: Alexandrov, Nickolai  
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
 ; TITLE OF INVENTION: Polypeptides Encoded Thereby  
 ; FILE REFERENCE: 2750-1590PUS2  
 ; CURRENT APPLICATION NUMBER: US/11/056,355B  
 ; CURRENT FILING DATE: 2005-02-14  
 ; PRIOR APPLICATION NUMBER: 60/544,190  
 ; PRIOR FILING DATE: 2004-02-13  
 ; NUMBER OF SEQ ID NOS: 119966  
 ; SEQ ID NO 2964  
 ; LENGTH: 428  
 ; TYPE: prt  
 ; ORGANISM: Zea mays subsp. mays  
 ; FEATURE:  
 ; NAME/KEY: peptide  
 ; LOCATION: (1)..(428)  
 ; OTHER INFORMATION: Ceres Seq. ID no. 12373378  
 US-11-056-355B-2964

Alignment Scores:  
 Pred. No.: 4.06e-06 Length: 428  
 Score: 148.00 Matches: 62  
 Percent Similarity: 38.1% Conservative: 18  
 Best Local Similarity: 29.5% Mismatches: 77  
 Query Match: 13.2% Indels: 53  
 DB: 7 Gaps: 10

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US-09-920-953-2 (1-598) x US-11-056-355B-2964 (1-428)
QY 5 TGCTGACAGCGG-----CCACGACACACAGAGCGGCGAAGCGG 49
Db 221 CysAlaArgThrArgAlaArgThrAlaProSerAlaProCysThrArgArgThr 240
QY 50 GATCGGGCGCAAGAGCTGTTGATGACCTGGGCGCGCAGAGGCGATGAGCTGCGG 109
Db 241 SerSerGlySerArgAlaCys-----247
QY 110 TTGACACCTTCTACGATAAGTGCTGG-----CTGACCCGAGCTGCTGC 154
Db 248 -----ProSerAlaAlaThrCysTrpArgTrpAlaAlaThrArgSerArgProThrSer 265
QY 155 CCTTCTTCGAGTCCCTGACATGCAAGAGCAGAGATGAAGCAGCTCAAGTTTCATGAGCT 214
Db 266 ProArgTrpGlyProTrpCysCysProSerProSer---SerCysSerSerSerArgAla 284
QY 215 TCGGTGTTGGCGGAGCAGACCAATACAGGGCCGAGCATGTACGACGACACGCCCATC 274
Db 285 CysCysSerAlaThrCysSerArgProArg-ProProArgArgArgArgProProGl 304
QY 275 TGGT-----CAAGGGCCAGCGCTGGACCCACCGCTTGTGACAGATCAAGCAGTACC 328
Db 304 nGlyThrProArgProProArgPro--ThrSerArgThrSerSerAlaArgSerSerThr 323
QY 329 TTGAGAGAGCTGCAAGAGA-----TGGCGGTCAACGAGAGATGTGATCC 373
Db 324 -----SerAlaCysThrArgProAlaAlaThrCysTrpSerThrCysArgAlaThrTrp 341
QY 374 AGACGCGCGCGAGTGGTGAGTCCACCGCGAGCAATTTGACTTNCACCAACTGCG 433
Db 342 AlaCysAlaThrProThrTrpArgProProAlaProArgCysThrAlaSerAlaThr--- 360
QY 434 CACCCAACTGATTTTCAATTAACCAACCCAGCGCTGATCCATTCATCGATTTTGAG 493
Db 361 -----ProGlnAlaAlaSerGlyThrSerTrpArg 371
QY 494 -----CGGGAGCGCCAGTTGCGGAGCGCGCCAGGGCGCGCCAGGAGCTGCA 541
Db 372 ThrTrpArgProArgAlaAlaSerAlaAlaAlaThrAlaSerGlySer---SerProSer 390
QY 542 AATCGTTTGCAGCGCTTGTGCA 565
Db 391 GlyArgAlaSerSerAlaThrAla 398

RESULT 2
US-11-056-355B-2962
; Sequence 2962, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 2962
; LENGTH: 544
; TYPE: prt
; ORGANISM: Zea mays subsp. mays
; NAME/KEY: peptide
; LOCATION: (1)-(544)
; OTHER INFORMATION: Ceres Seq. ID no. 12373376
US-11-056-355B-2962

Alignment Scores:
Pred. No.: 4.28e-06 Length: 544
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Score: 148.00 Matches: 62
Percent Similarity: 38.1% Conservative: 18
Best Local Similarity: 29.5% Mismatches: 77
Query Match: 13.2% Indels: 53
DB: 7 Gaps: 10

US-09-920-953-2 (1-598) x US-11-056-355B-2962 (1-544)
QY 5 TGCTGACAGCGG-----CCACGACACACAGAGCGGCGAAGCGG 49
Db 337 CysAlaArgThrArgAlaArgThrAlaProSerAlaProCysThrArgArgThr 356
QY 50 GATCGGGCGCAAGAGCTGTTGATGACCTGGGCGCGCAGAGGCGATGAGCTGCGG 109
Db 357 SerSerGlySerArgAlaCys-----363
QY 110 TTGACACCTTCTACGATAAGTGCTGG-----CTGACCCGAGCTGCTGC 154
Db 364 -----ProSerAlaAlaThrCysTrpArgTrpAlaAlaThrArgSerArgProThrSer 381
QY 155 CCTTCTTCGAGTCCCTGACATGCAAGAGCAGAGATGAAGCAGGTCAAGTTTCATGAGCT 214
Db 382 ProArgTrpGlyProTrpCysCysProSerProSer---SerCysSerSerSerArgAla 400
QY 215 TCGGTGTTGGCGGAGCAGACCAATACAGGGCCGAGCATGTACGACGACACGCCCATC 274
Db 401 CysCysSerAlaThrCysSerArgProArg-ProProArgArgArgArgProProGl 420
QY 275 TGGT-----CAAGGGCCAGCGCTGGACCCACCGCTTGTGACAGATCAAGCAGTACC 328
Db 420 nGlyThrProArgProProArgPro--ThrSerArgThrSerSerAlaArgSerSerThr 439
QY 329 TTGAGAGAGCTGCAAGAGA-----TGGCGGTCAAGCAGAGATGTGATCC 373
Db 440 -----SerAlaCysThrArgProAlaAlaThrCysTrpSerThrCysArgAlaThrTrp 457
QY 374 AGACGCGCGCGAGTGGTGAGTCCACCGCGAGCAATTTGACTTNCACCAACTGCG 433
Db 458 AlaCysAlaThrProThrTrpArgProProAlaProArgCysThrAlaSerAlaThr--- 476
QY 434 CACCCAACTGATTTTCAATTAACCAACCCAGCGCTGAGCGCTCATTCATCGATTTTGAG 493
Db 477 -----ProGlnAlaAlaAlaSerGlyThrSerTrpArg 487
QY 494 -----CGGGAGCGCCAGTTGCGGAGCGCGCCAGGGCGCGCCAGGAGCTGCA 541
Db 488 ThrTrpArgProArgAlaAlaSerAlaAlaAlaThrAlaSerGlySer---SerProSer 506
QY 542 AATCGTTTGCAGCGCTTGTGCA 565
Db 507 GlyArgAlaSerSerAlaThrAla 514

RESULT 3
US-11-056-355B-7635
; Sequence 7635, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 7635
; LENGTH: 212
; TYPE: prt
; ORGANISM: Zea mays subsp. mays
; NAME/KEY: peptide
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LOCATION: (1)-(212)  
OTHER INFORMATION: Ceres Seq. ID no. 12408188  
US-11-056-355B-7635

Alignment Scores:  
Pred. No.: 2,9e-05 Length: 212  
Score: 138.50 Matches: 68  
Percent Similarity: 39.8% Conservative: 14  
Best Local Similarity: 33.0% Mismatches: 74  
Query Match: 12.3% Indels: 51  
DB: 7 Gaps: 12

US-09-920-953-2 (1-598) x US-11-056-355B-7635 (1-212)

```
QY 576 TGGCTCTTCAATGACGAGGCTGGCAACAGATTGTCAGGCTCTGGGCCCC---TGG 520
DB 16 TrpLeuHis-----ArgTrpProProArgAlaHisSerTrpAlaProAlaTrp 32
QY 519 -----GGCGCTCGGCAACTGGCGTCCCGCTCCAAATCGATGGAATGAGCGCTCAGG 466
DB 33 ArgThrArgArgHisArgThrGlyAla-----Ser-Trp---ProGlySerGI 47
QY 465 CTGGGTTGGGTTAATAAATCAGTTGGTGGCGCAGTTGTTGGGNAAGTCAAAATTCGTC 406
DB 47 ySerGlyTrpAlaAlaArgArgSerLeu-LeuArgArgTrp-----A 62
QY 405 GCGGTGGACTCCACACTCCGGCGGCGTGTGGATACATCTCTGTCAGCCCATC-- 348
DB 62 rArgHisArgProProLeuThrGlyArgCysGlySerProAlaProTrpArgProThrT 82
QY 347 -----TCTTGACGCTCTCTCCAA 329
DB 82 hrTrpThrAlaArgTrpSerAlaThrThrGlySerThrArgSerValSerGlySerPro- 101
QY 328 GGTACTGCTTGATCTGTCAAAATGG---CGGTGGTCCAGGCGGTGGCCCTTGACAGAT 272
DB 102 --TrpSerThrCysSerSerTrpThrArgTrpThrArgTrpProArgMetArgP 121
QY 271 GGGCTGTGCGTGCACATGCTTCGGCCCTTGTATGTTGCTCTCGCCAAACAGAAC 212
DB 121 roAlaAlaSerSer-----AlaProGlySerSerProProLysSerSerP 136
QY 211 TCATGAACCTGACCTGCTTCATCTTCTGCTTGTGATGTCAGGACTCGAAGAGGCA 152
DB 136 roProArgCysSerProThrAlaArgCysSerAlaSerSer-----GlyS 151
QY 151 GCAGCTCCGGTCCAGCACCTTATCGTAGAAGTGTCAACCGCAGCTTCATCGCTT 92
DB 151 arAlaSerAlaSerSerThrAlaAla-GlyProCysSerProProSerAla----- 168
QY 91 CTGCCGCCAGGTCATCAACAGCTTCTTGGCCCGCATCCCGCTTCGCCGCTCTCTG 32
DB 169 -----ProSerProSerSerGlySerProAlaSerProGlyArgThrProAlaArg 185
QY 31 TGGTCTGGTGG 20
DB 186 TrpSerTrpTrp 189
```

## RESULT 4

US-10-953-349-30500  
Sequence 30500, Application US/10953349  
Publication No. US20060107345A1  
GENERAL INFORMATION:  
APPLICANT: ALEXANDROV, Nikolai et al.  
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
TITLE OF INVENTION: ENCODED THEREBY  
FILE REFERENCE: 2750-1579PUS2  
CURRENT APPLICATION NUMBER: US/10/953,349  
CURRENT FILING DATE: 2004-09-30  
NUMBER OF SEQ ID NOS: 40252  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 30500  
LENGTH: 214

TYPE: PRT  
ORGANISM: Triticum aestivum  
US-10-953-349-30500

Alignment Scores:  
Pred. No.: 5,09e-05 Length: 214  
Score: 136.00 Matches: 57  
Percent Similarity: 37.4% Conservative: 19  
Best Local Similarity: 28.1% Mismatches: 74  
Query Match: 12.1% Indels: 53  
DB: 6 Gaps: 9

US-09-920-953-2 (1-598) x US-10-953-349-30500 (1-214)

```
QY 530 GGGCCCCCTGGCGCGCTCGGCAACTGGCGCTCCCGCTCAAAATCGATGGAATGAGCGC 471
DB 17 GlyArgGlyGlyGlnAlaArgArgSerGluGlnProTrpLeuArgArgTrpProArg 36
QY 470 -----TCAGGCTGGGTTGG---GTTAATGAAATCAGTTGGTGGCGCAGTTG 426
DB 37 ArgAlaArgSerSerGlyProGlyTrpArgThrArgArgArgThrGlyAlaSerTrp 56
QY 425 TTGGGNAG----- 417
DB 57 ArgGlySerAlaSerAlaArgArgProArgArgArgArgProArgProArgPro 76
QY 416 -----TCAAAATTCGTCGGCGGTGGACTCCACACTCCGGCGCGGTGC 375
DB 77 ProThrGlyArgCysGlySerProAlaArgArgProSerThrSerThrAlaArgSer 96
QY 374 TGGATCATCTCTGTCAGCCCATCTCTTGCAGCGTCTCTCCAGGCTACTGCTTGATC 315
DB 97 SerAlaThrThrAlaSerThrPro---SerAlaSerGlySerProArgSerThrCysSer 115
QY 314 TTGCAAAAGTGGCGTGTGCAGGCGGTGGCCCTTGACCAGATGGCGGTGTCGCTGATC 255
DB 116 ThrThrTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrp 133
QY 254 ATGCTTCGGCCCTTGTATGTTGCTCTGCTCCG-----CCAAACACGAAAGTCTATG 207
DB 134 -----SerAlaProGlySerArgThrProThrSerSerProPro 146
QY 206 AACTTGACCTGCTTCATCTTCTGCTTGTGATGTCAGGACTCGAAGAGGCGAGCAGC 147
DB 147 ArgSerSerProThrProArgCysSer-----AlaSerArgGlySerAla 161
QY 146 TCCGGTTCAGCAGCAGCTTATCGTAGAAGTGTCAACCGCAGCTTCATGCTTCTGCG 87
DB 162 SerAlaSerSerSerThrAlaAla-GlyProCysSerProProSerAla----- 177
QY 86 CCGCCCGAGGTTCATCAACAGCTTCTTGGCCCGCATCCCGCTTCGCCGCTCTCTGTG 27
DB 178 ---ProSerProSerSerGlySerProAlaSerProGlyArgThrProAlaArgTrpSe 196
QY 26 CTGGTGG 20
DB 196 rTrpTrp 198
```

## RESULT 5

US-11-056-355B-51768  
Sequence 51768, Application US/11056355B  
Publication No. US20060150283A1  
GENERAL INFORMATION:  
APPLICANT: Brover, Vyacheslav  
APPLICANT: Alexandrov, Nikolai  
TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING  
TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY  
FILE REFERENCE: 2750-1590PUS2  
CURRENT APPLICATION NUMBER: US/11/056,355B  
CURRENT FILING DATE: 2005-02-14  
PRIOR APPLICATION NUMBER: 60/544,190  
PRIOR FILING DATE: 2004-02-13  
NUMBER OF SEQ ID NOS: 119966

; SEQ ID NO 51768  
; LENGTH: 210  
; TYPE: prt  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(210)  
; OTHER INFORMATION: Ceres Seq. ID no. 15177853  
US-11-056-355B-51768

Alignment Scores:  
Pred. No.: 0.000304 Length: 210  
Score: 128.00 Matches: 55  
Percent Similarity: 36.9% Conservative: 20  
Best Local Similarity: 27.1% Mismatches: 75  
Query Match: 11.4% Indels: 53  
DB: 7 Gaps: 9

US-09-920-953-2 (1-598) x US-11-056-355B-51768 (1-210)

```
QY 530 GGGCCCCCTGGCGCGCTCGGCAACTGGCGCTCCCGCTCCAAATCGATGAATGAGCGC 471
Db 13 GlyArgGlyGlyGlnAlaArgSerGluGlnProThrLeuArgArgTrpProArg 32
QY 470 -----TCAGGCTGGGTTGG--GTTAATGAAATCAGTTGGGTGGCGACTTG 426
Db 33 ArgAlaArgSerGlyProGlyTrpArgThrArgArgArgThrGlyAlaSerTrp 52
QY 425 TTGGGNAAG----- 417
Db 53 ArgGlySerAlaSerAlaArgArgProArgArgArgProArgProArgPro 72
QY 416 -----TCAATTCCTGGGGTGGACTCCACCACTCCGGGGCGGTGC 375
Db 73 ProThrGlyArgCysGlySerProAlaArgArgProSerThrSerThrGlyArgSer 92
QY 374 TGGATCATCTCTGTTGAGCCCATCTCTTGCAGCGTCTCTCAAGTACTGCTTGCATC 315
Db 93 SerAlaThrThrAlaSerThrPro--SerAlaLeuGlySerProArgSerThrCysSer 111
QY 314 TTGTCAAGTGGCGGTGGTCCAGGCCGTGGCCCTTGACCATGGCGCTGTGCGTCTGATC 255
Db 112 ThrThrTrpThrProTrpThrArgThrTrpProArgThr--TrpArgAlaArgSer-- 129
QY 254 ATGCTTCGGCCCTTGATTGCTGCTCGG-----CCAAACACAGAGCTCATG 207
Db 130 -----SerAlaProGlySerArgThrProThrSerSerProPro 142
QY 206 AACTTGACCTGCTCATCTTCTGCTCTTGATGTCCAGGACTCGAAGAGGGCAGCAGC 147
Db 143 ArgSerSerProThrProArgCysSer-----AlaSerArgGlySerAla 157
QY 146 TCGGGGTCCAGCAGCCTTATCTAGAGGTGTCACCGCCAGCTTCATGCTTCTGCG 87
Db 158 SerAlaSerSerThrValAla-GlyProCysSerProProSerAla----- 173
QY 86 CCGCCAGGTCATCAACAGCTTCTTGGCCCGCATCCCGCTCCCGCTCTGCTGCTG 27
Db 174 ----ProSerProSerGlySerProAlaSerProGlyArgThrProAlaArgTrpSe 192
QY 26 CTGGTGG 20
Db 192 rtrpTrp 194
```

## RESULT 6

US-10-953-349-28428  
; Sequence 28428, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; TITLE OF INVENTION: ENCODED THERBY  
; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 28428  
; LENGTH: 358  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (306)..(306)  
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
US-10-953-349-28428

Alignment Scores:  
Pred. No.: 0.000939 Length: 358  
Score: 123.50 Matches: 62  
Percent Similarity: 33.5% Conservative: 9  
Best Local Similarity: 29.2% Mismatches: 62  
Query Match: 11.0% Indels: 79  
DB: 6 Gaps: 9

US-09-920-953-2 (1-598) x US-10-953-349-28428 (1-358)

```
QY 21 CACACACACACACAGACGCGGAGCGGATCGGGCGCAAGAGCTGTTGTATGACCT 80
Db 41 HisSerHisAspArg-----Ala 46
QY 81 GGGCGCGGAGAGGATGAAGCTGCGGTTGACAC----- 116
Db 47 GlyArgArgArgProHisSerIleProArgArgHisAspAlaValArgLeuGlnArgArg 66
QY 117 CTTTACGATAGGTCTGCTGCTGACCGGAGCTGCTGCTTCTTGGAGTCCCTGGACAT 176
Db 67 ProIleArgArgGlyAlaGly-----ArgArgValProIlePro 79
QY 177 GCAAGAGCAGAGATGAAGCAGCTCAAGTTCAAGTTCGTCTGTTGGCGGAGCAGA--- 233
Db 80 ArgArgProGluAlaProAlaGlyGluValArgAlaGlyArgAlaProArgProArgArg 99
QY 234 -----CCAATACAGGGCGCGAAGCAT----- 254
Db 100 ValArgGlnGlyLeuProGlyGlnGlyHisProHisGlyProGlyArgGlyHisGlnVal 119
QY 255 -----GTACACGCGACA 266
Db 120 ValProGlnProAlaGlyArgArgAlaArgGlyGlyGlyLeuArgValArgArgHis 139
QY 267 CGCCCATCTGTTCAAGGGCCAGCGCTGGACCCACCGCCACTTTTGACAGATCAAGCAGTA 326
Db 140 ArgAlaGlyGlyHisProGlnProProAlaProPro----- 152
QY 327 CTTTGAGAGAGCGCTCAAGAGATGGCGTCAAGCAGAGA-----TGTGATCCA 374
Db 153 ProArgArgGluAlaProArgAspSerArgHisAlaGlnGluGlyProLeuCysProArg 172
QY 375 GCACGCGCGCGAGTGGTGGAGTCCACCGCGGACGAATTTGACTTCCCAACACTGCGGC 434
Db 173 ProArgArgArg-----ArgArgAlaValLeuAlaArgArgLeuArg 186
QY 435 ACCCACTGATTTCATTAAACCAACCCAGCGCTGAGCGCTCATTCATCGATTTTGAGC 494
Db 187 ArgPro-----HisAspGlyGlyProArgAlaAlaLeuLeuProThrAlaArgVal 203
QY 495 GGGGAGCGCGAGTTGCCGAGCGCGCCCGAGGGGCGCC 530
Db 204 GlyArgProValLeuProLeuProArgArgLeuPro 215
```

## RESULT 7

US-11-056-355B-3621  
; Sequence 3621, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:

APPLICANT: Brover, Vyacheslav  
APPLICANT: Alexandrov, Nickolai  
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
FILE REFERENCE: 2750-1590PUS2  
CURRENT APPLICATION NUMBER: US/11/056,355B  
PRIOR FILING DATE: 2005-02-14  
PRIOR APPLICATION NUMBER: 60/544,190  
NUMBER OF SEQ ID NOS: 119966  
SEQ ID NO 3621  
LENGTH: 375  
TYPE: prt  
ORGANISM: Zea mays subsp. mays  
FEATURE:  
NAME/KEY: peptide  
LOCATION: (1)..(375)  
OTHER INFORMATION: Ceres Seq. ID no. 12414168  
US-11-056-355B-3621

Alignment Scores:  
Pred. No.: 0.00208 Length: 375  
Score: 120.00 Matches: 56  
Percent Similarity: 37.2% Conservative: 21  
Best Local Similarity: 27.1% Mismatches: 92  
Query Match: 10.7% Indels: 38  
DB: 7 Gaps: 8

US-09-920-953-2 (1-598) x US-11-056-355B-3621 (1-375)

QY 5 TGCCTGCAGACGCGGCACACAGACAGACGCGGAGCGGATCGGGCGCAAGA 64  
DB 172 CysArgAlaThrArgProAlaAlaProSerArgThrThrSerProCysAla----- 188

QY 65 AGCTGTTGATGACCTGCGCGCGGCGGAGAGGATGAAGCTGCGGTGACACTTCTACG 124  
DB 189 -----SerValAlaArgProArgThrTrpProProSerPro----- 200

QY 125 ATAAGGTGCTGCTGACCGGAGCTGCTCCCTCTTCGAGTCCCTGGACATGCAAGAGC 184  
DB 201 -----CysGlyAspThrSerSerCysHisSerSerAlaAlaThrArgAlaArgGly 218

QY 185 AGAAGATGAAGCAGCTCAAGTTTCATGAGCTTCGTGTTGTCGCGAGCAGACCAATACAAG 244  
DB 219 ArgArgProSerAlaProThrLeuSerSerThrGlyProSerThrThrAlaThrGly 238

QY 245 GCCGAAGCATGTACGACGACACAGCCCATCTCGTCAAGGCGCCGCTGGACACCGCC 304  
DB 239 AlaCysArgCys-----ArgArgAlaProArgProThrThrPro 251

QY 305 ACTTTGACAAGATCAAGCAGTACCTTGGAGACGCTGCAAGAGATGGCGTCAAGCAGG 364  
DB 252 TrpProThrArgSerAlaProAlaArg-----ArgArgTrpThrProSer--- 266

QY 365 ATGTGATCAGACGCGCGGAGTGGTGGAGTCCACCGCG-----ACGAATTG 415  
DB 267 -----SerSerArgProPro-----TrpSerSerAlaAlaAlaThrSerSerThr 282

QY 416 ACTTNCACCAACTGCGCACCCCACTGATTTCATTAAACCAACCCAGCTGAGCGCT 475  
DB 283 ThrAlaProSerThrThrProProGlySerGlyProProGlySerProSerTrpSerGly 302

QY 476 CATTCATCGATTGAGCGGGAGCG-----CCAGTTCGCCAGCGC 517  
DB 303 ThrSerThrAlaSerSerThrAlaSerProSerThrProGlyProThrProPro 322

QY 518 GCCCAGGGGCCAGGAGCTCAATCGTTTGGCAGCGCTTGCATTTGAAGAGCCAT 577  
DB 323 SerSerCysAlaSerSerSerAlaSerSerThrProThrAlaAlaSerThrSerThrAsp 342

QY 578 CAGCCATTTTCGACCAAGCC 598  
DB 343 ThrSerValSerAsnSerSer 349

## RESULT 8

US-11-056-355B-3480  
Sequence 3480, Application US/11056355B  
Publication No. US20060150283A1  
GENERAL INFORMATION:  
APPLICANT: Brover, Vyacheslav  
APPLICANT: Alexandrov, Nickolai  
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
FILE REFERENCE: 2750-1590PUS2  
CURRENT APPLICATION NUMBER: US/11/056,355B  
PRIOR FILING DATE: 2005-02-14  
PRIOR APPLICATION NUMBER: 60/544,190  
PRIOR FILING DATE: 2004-02-13  
NUMBER OF SEQ ID NOS: 119966  
SEQ ID NO 3480  
LENGTH: 309  
TYPE: prt  
ORGANISM: Zea mays subsp. mays  
FEATURE:  
NAME/KEY: peptide  
LOCATION: (1)..(309)  
OTHER INFORMATION: Ceres Seq. ID no. 12367975  
US-11-056-355B-3480

Alignment Scores:  
Pred. No.: 0.00348 Length: 309  
Score: 117.50 Matches: 75  
Percent Similarity: 36.7% Conservative: 15  
Best Local Similarity: 30.6% Mismatches: 86  
Query Match: 10.5% Indels: 69  
DB: 7 Gaps: 13

US-09-920-953-2 (1-598) x US-11-056-355B-3480 (1-309)

QY 15 CCGCGCCACCAACGAC-----CACAGACGCGGAGCGGATCGGGCGCAAGAAGCT 68  
DB 57 ArgGlyHisArgHisProSerHisArgProLeuAlaSerValArgGln----- 72

QY 69 GTTTGATGACCTGGCGCGCGGAGGATGAAGCTGCG----- 107  
DB 73 -----ArgArgArgArgGlyArgAlaGlyArgGlyGlyArgGlyGlu 87

QY 108 ---GTTTACACCTCTACGA-----TAAGTGCT 134  
DB 88 ProGlyLeuGlyLeuLeuArgGlyArgGlyProArgArgAlaArgAspHisGlyAla 107

QY 135 GCGTACCGCGGAGCTGCTGCGCTTCTTCAGTCCCTGGACATGCA-----AGAGCA 185  
DB 108 ArgAspGlyGlyAlaAlaArgValLeuArgAlaAlaGlyArgAlaGlyArgAla 127

QY 186 GAAGATGAAGCAGCTCAAGTTTCATGAGCTTCGTGTTGCGGAGCAGACCA----- 236  
DB 128 GluGluArgGlyGlyAlaAlaArgValLeuArgValGlyAlaHisGlnGluArgGly 147

QY 237 ATACAGGCGCGAGCATGTACGACGACAGCCCATCTGTCAGGCGCCGCTGGA 296  
DB 148 LeuGluGlyGlyValArgProArgAlaAlaAlaAlaAlaGlyCysArgGlyArg 167

QY 297 CCACCGCCACTTTCACAGATCAACAGCAGTACT-----TGGAGAGACGCT 341  
DB 168 ArgArgAlaArgValArgGluGlnValAlaProGlySerAlaGlyLeuGlnArgGlyAla 187

QY 342 GCA-----AGAGATGGCGGT-----CAAGCAGGATGTGATCCAGCA 377  
DB 188 GlyGlyValArgGlnSerAspGlyArgAlaGlyValGlnAlaAlaGlyAlaAsp--ArgS 207

QY 378 CGCGCGGAGTGTGGAGTCCACCGCGAGCAAT---TTGACTTNCACCAACTGCGC 434  
DB 207 erGluProGluAlaGluAlaArgProAlaAlaArgLeuLeuGlnGlyProAspAspLeuH 227

QY 435 ACCCAACTGATTTTCATTAAACCCACCCAGCGCTCATTCATCGATTTTGAC 494



; GENERAL INFORMATION:  
 ; APPLICANT: National Institute of Agrobiological Sciences.  
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
 ; APPLICANT: The Institute of Physical and Chemical Research.  
 ; APPLICANT: Foundation for Advancement of International Science.  
 ; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
 ; FILE REFERENCE: MOA-A0205YI-US  
 ; CURRENT APPLICATION NUMBER: US/10/449,902  
 ; PRIOR FILING DATE: 2003-05-29  
 ; PRIOR APPLICATION NUMBER: JP 2002-203269  
 ; PRIOR FILING DATE: 2002-05-30  
 ; PRIOR APPLICATION NUMBER: JP 2002-383870  
 ; PRIOR FILING DATE: 2002-12-11  
 ; NUMBER OF SEQ ID NOS: 56791  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 40564  
 ; LENGTH: 317  
 ; TYPE: PRT  
 ; ORGANISM: Oryza sativa  
 ;  
 ; US-10-449-902-40564

Pred. No.:	Score:	Length:
0.00612	317	
115.00	Matches:	48
Percent Similarity:	Conservative:	12
Best Local Similarity:	Mismatches:	74
Query Match:	Indels:	10 30
DB:	Gaps:	7

US-09-920-953-2 (1-598) x US-10-449-902-40564 (1-317)

```

Qy   439 TGGGTGCGCAGTGTGGNAAAGTCAAATTCGTGCGGGTGGAATCCACCACTCCGGCGG 380
Db   129 TrpileLysSerPheValVal-----TipPheCysSerAlaAlaArg 143
Qy   379 CGTCTGTGCATCATCTTCGCTTGAGCCCATCTTTGACGGCTCTCTCCAAGT----- 326
Db   144 ArgThrTrpCysAlaProAlaAlaAlaAlaAlaThrThrAlaSerSerAlaAlaPro 163
Qy   325 -----ACTGCTTGATCTTGTCAAAGTGCGGTGGTCCAGGCCGTGGCCCTTGACC 275
Db   164 ArgThrProThrAlaProSerSerTrpThrProSerSerAlaProArgTrpArgAlaPro 183
Qy   274 GATGGCGGTGCGCTGCFACATGCTTCGGC-----CCTTGATTGCTCTG 230
Db   184 ThrArgArgThrAlaAlaThrAlaThrSerCysThrAlaArgProProSerThrSerAla 203
Qy   229 CTCGCCAACACAGAAGCTCATGAATTGACTGCTTCATCTTCGCTCTTGCTATGTCCA 170
Db   204 ArgAlaArgAlaArgProAla-----ProAlaArgThrProAlaAlaSerAla 220
Qy   169 GGGACTCGAAGAAGGCGACGAGCT-----CCGGGTGACCCAGCACCTTATCGTAG 119
Db   221 AlaArgArgArgSerSerAlaThrSerProProThrThrProGlyProSerArgArg 240
Qy   118 -----AGGTGTCAAACGCCGACGCTTCATGCTTCGCGCGCCCGCCAGGTGCAT 74
Db   241 SerAlaThrArgSerArgAlaGlySerProCysArgCys-----ProGlygly 256
Qy   73 CAACACGCTTCTTCGGCCGCGCATCCCGCTTCGCGCGTCTCTGTGTGCTGTGGTGGCGG 14
Db   257 AlaThrSerSerSerGlyArgThrThrAlaProCysSerTrpTrpCysProArgProArg 276
Qy   13 CTGCGAGCGCG 2
Db   277 AlaAlaSerAla 280
  
```

Alignment Scores:

RESULT 13

US-11-056-355B-16356

; Sequence 16356, Application US/11056355B

; Publication No. US20060150283A1

; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav

QY 30 GGTGCTGGTGGCCG 17  
Db 269 -----TrrTrrPro 271

## RESULT 14

US-11-056-355B-16355  
; Sequence 16355, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 16355  
; LENGTH: 355  
; TYPE: prt  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(355)  
; OTHER INFORMATION: Ceres Seq. ID no. 12405304  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (259)..(259)  
; OTHER INFORMATION: Xaa is any aa, unknown or other  
US-11-056-355B-16355

Alignment Scores:  
Pred. No.: 0.011 Length: 355  
Score: 112.50 Matches: 59  
Percent Similarity: 32.5% Conservative: 8  
Best Local Similarity: 28.6% Mismatches: 56  
Query Match: 10.0% Indels: 83  
DB: 7 Gaps: 13

US-09-920-953-2 (1-598) x US-11-056-355B-16355 (1-355)

QY 555 GCTGGCAACGATTGCGCC-----TCCTGGGCCCCCTGGGCGCGCTCGGCACTGGC 502  
Db 127 AlAGlySerArgGlyThrGlyArgProSerTrpSerProArgThrArgSerTrpThrGly 146  
QY 501 -----GCTCCCGCTCA-----AAA 487  
Db 147 ProThrCysPheSerCysProArgSerArgProSerThrGlyProArgAlaSerCysArg 166  
QY 486 TCGATGGAATGAGCGCTCAGGCTGGGGTTGGGTTAATGAAATCAGTTGGGTGCGCAGTT 427  
Db 167 :ArgAlaArgProArgSerGlyThrArgTrp-----176  
QY 426 GTTGGGNAAGTCAATTCGTCCGGGTGGATCCACACTCCGGCGGCGTGTGATCAAC 367  
Db 177 -----ArgAlaThrLeuProArgCys---SerAlaTrpProProAlaCysTrp-----191  
QY 366 ATCTGCTTGACGCCCATCTCTTGACGGCTCTCTCCAGGACTCTGCTTGATCTTGTCAA 307  
Db 191 -----191  
QY 306 GTGGCGGTGGTCCAGCGCTGGCCCTTGACACAGATGGCGTGTGGTGTGCTATCCTTCG 247  
Db 192 -----ArgProTrpProArgThr---TrpAlaTrpArgThr-----202  
QY 246 GCCCTGTATTGGTCTGCTCCGCCAAACACGAAGCTCATGAACCTGCTGCTCATCTT 187  
Db 203 -ProArgGlyTrpProGlySerPro-ThrArgArg-----ProCysAlaSerT 218  
QY 186 CTGCTCTTGCATGTCACGGGACTTCAAGA---AGGGCAGCAGCTCGGGTACGCGAGC 130  
::

Db 218 hrThr-----ThrArgAlaAlaArgThrAlaGlyAlaGlyCysTrpAlaC 233  
QY 129 CTTATCGTAGAAGGTGTCAACCCGACGCTTCATCCCTTCTGCGC-----86  
Db 233 ysArgArgThrArgThrProProAlaSerArgCysCysSerArgSerAlaProSerArgG 253  
QY 85 -----CGCCAGGTTCATCAACAGCTTCTTGGCGCCGCGCATCCGCTTCCGCGCTCTCTGT 31  
Db 253 lyCysArgSerGlyGly\*\*\*AlaArgGlySerAlaSerThrProSerProGluArg-----271  
QY 30 GGTGCTGGTGGCCG 17  
Db 272 -----TrrTrrPro 274

## RESULT 15

US-10-953-349-33290  
; Sequence 33290, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; TITLE OF INVENTION: ENCODED THERBY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 33290  
; LENGTH: 199  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
US-10-953-349-33290

Alignment Scores:  
Pred. No.: 0.0108 Length: 199  
Score: 112.00 Matches: 58  
Percent Similarity: 34.1% Conservative: 14  
Best Local Similarity: 27.5% Mismatches: 78  
Query Match: 10.0% Indels: 61  
DB: 6 Gaps: 11

US-09-920-953-2 (1-598) x US-10-953-349-33290 (1-199)

QY 536 GCTCCTGGGCGCCCT-----GGCGCGCTCGGCACTGGCGCTCCCGCTCAAAAT 486  
Db 8 SerProLeuProProLeuLeuSerSerArgProThrHisLeuLeuAlaProAlaProGly 27  
QY 485 CGATGGAATGAGCGCTCAGGC-----TGGGGT 459  
Db 28 LysTrpArgProArgCysGlyArgCysCysTrpTrpTrpProCysArgArgTrpArg 47  
QY 458 TGGTTAATGAAATCAGTTGGGTGCGC-----431  
Db 48 TrpProArg-ThrAlaProTrpArgArgArgProArgArgArgArgArgArgTrpAr 67  
QY 430 -----AGTTGTTGGGNAAGTCAAAATTCGTGCG-----GG 402  
Db 67 gCysSerAlaAlaThrSerCysArgGlyAlaCysCysArgArgGlySerArgArgSerGl 87  
QY 401 GTGACATCCACCACTCCGGCGG---CGTGCTGGA---TCACATCCTGCTTGACGCCCATC 348  
Db 87 yThrTrpProProArgGluArgSerArgProGlyTrpThrArgProAlaArgAlaSe 107  
QY 347 TCTTTCAGCGCTCTCTCCAAAGGTACTGCTTGTATCTTGTCAAAGTGGCGGTGGTCCAGGCCG 288  
Db 107 xArgSerAlaSer-----AlaThrTrpProProSerProGlySerSerAlaProAlaAr 125  
QY 287 TGGCCCTTGACCAAGATGGCGGTGCTGCTGACAC-----TGCTCGGCCCTTGATTGG 234  
Db 125 gSerProThrSerProAlaSerProArgArgThrSerSerCysGlySerProSer-----143  
QY 233 TCTGCTCGGCCAAACAGAGCTCATGAACCTTGACCTGCTTCATCTTCTGCTCTTTCATG 174  
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Db 144 -----ThrThrSerArgSerThrSerProProProAlaSerSerThrThrSerAl 161
Qy 173 TCCAGGGACTCGAAGAGGCGAGCTCCGGGTCCAGCCAGCACCTTATCGTAGAAGGTG 114
Db 161 a---SerSerArgSerThrSerArgSerPro-----170
Qy 113 TCAACCGCCAGCTTCATGCCTTCTCGCGCGCCAGGTCAACAAACAGCTTCTTGGCCCG 54
Db 171 -----SerSerThrArgArgProAlaArgProThrArgSerCysArgSe 186
Qy 53 CATCCCGCTTCGCCGCTCTCTGTGTGTGG 23
Db 186 rPheLeuIleLeuAlaSerLeuSerArgTrp 196

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Search completed: August 11, 2006, 10:35:56  
 Job time : 23 secs